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REMARKS

Applicants submit that the DNA sequence of Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) in Figure 13A contain a typographical error between nucleotide positions 1169 and 1171. The corresponding amino acid sequence of Pfu DNA polymerase D141A/E143A / V93R (SEQ ID NO: 44) and PFU DNA polymerase D141A/E143A/ V93E (SEQ ID NO: 46) is shown in Figure 13B as the following sequence ---SYTGG--- (underlining denotes amino acid position 387) which is identical to the amino acid sequence of wild type Pfu DNA polymerase in Figure 20. The presence of Glycine at position 387 is therefore consistent with the sequence GGT between nucleotide positions 1169 and 1171 not the sequence CCN as shown in the originally filed Figure 13A. Hence, the Pfu DNA polymerase D141A/E143A / V93R mutant (SEQ ID NO: 31) and PFU DNA polymerase D141A/E143A/ V93E mutant (SEQ ID NO: 32) sequence in Figure 13A are amended to show the wild type sequence 'GGT' instead of 'CCN' between nucleotide positions 1159 and 1161. No new matter is added.

Applicants submit that the DNA sequence encoding Sac7d- Taq fusion protein (SEQ ID NO: 128) in Figure 20 contains typographical errors between nucleotide positions 230 and 232, 343 and 351, and 778 and 780.

Applicants submit that the sequence 'OTC' between positions 142 and 144 within the Taq DNA polymerase sequence and the corresponding amino acid 'X' in Figures 17B, 17C, 17U, 17V, 17NN, 17OO and 17FFF are typographical errors. The wild type DNA sequence at this location is 'GTC' and the corresponding amino acid is Valine as reported in SEQ ID NO:1 of U.S. Patent No. 5,466,591 (Abramson et a., filed February 23 1993) which is incorporated by reference on page 3, line 4 of the present application. Hence the Taq DNA polymerase nucleotide (SEQ ID NO:65) and amino acid (SEQ ID NO: 66) sequences in Figures 17B, 17C, 17U, 17NN, 17OO and 17FFF are corrected to show the wild type sequence 'GTC' and the corresponding amino acid 'Valine' between positions 142 and 144.

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Applicants submit that the amendments of the figures are only made to correct typographical errors and to introduce SEQ ID Nos next to the corresponding nucleotide and amino acid sequences depicted in the Figures and that these amendments do not introduce any new matter.

Date:

Movember 4,2004

Respectfully submitted,

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Amendments to the Drawings:

Applicants further propose amendments to Figures 10, 13 A-B, 14, 17A-17S, 17T-17LL, 17MM-17DDD, 17EEE-17RRR, 18, 19 and 20 herein attached.



FIGURE 10

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAgATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [6]5)

V93E#2

5'-CTTTTTCTCTAATAqTqqqTTCATCTTqqqqATqTTC-3' (SEQ ID NO: [7]6)

V93R#1

5'-gAACATCCCCAAgATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [8]7)

V93R#2

5'-CTTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: [9]8)

V93N#1

5'-gAACATCCCCAAgATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [10]9)

V93N#2

5'-CTTTTTCTCTAATAgTggggTTATCTTgggggATgTTC-3' (SEQ ID NO: [11]10)

V93H#1

5'-gAACATCCCCAAgATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [12]11)

V93H#2

5'-CTTTTTCTCTAATAgTggggTgATCTTgggggATgTTC-3' (SEQ ID NO: [13]12)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAgATNNKCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [14]13)

V93K#1

5'-gAACATCCCCAAgATAAACCCACTATTAgAg-3' (SEQ ID NO: [15]14)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: [16]15)

QCM#1 5'-(Phosphate)gAACATCCCCAAgATgCACCCACTATTAgAgAAAAAg-(SEQ ID NO:

[17]16)'

Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAgATgACCCCACTATTAgAgAAAAAg-3'(SEQ ID

NO: [18]<u>17</u>)

Aspartic Acid

Marked-Up Version

QCM#3 5'-(Phosphate)gAACATCCCCAAgATTgCCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: [19]<u>18</u>) Cysteine

QCM#4 5'-

(Phosphate)gAACATCCCCAAgATATACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: [20]19)

Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAgATATgCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: [21]<u>20</u>)

Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAgATTTCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: [22]<u>21</u>)

Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAgATCCTCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: [23]22)

Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAgATAgCCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 23)

Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAgATACACCCACTATTAgAgAAAAAg- 3' (SEQ ID

NO: 24)

Threonine

QCM#10 5'-(Phosphate)gAACATCCCCAAgATTACCCCACTATTAgAgAAAAAg-3' (SEQ ID

NO: 25)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAgATTggCCCACTATTAgAgAAAAAg-3'

(SEQ ID NO: 26)

Tryptophan

MARKED UP VERSION OF AMENDED FIGURE 13A

Please replace Figure 13A with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13A.

FIGURE 13A

PFU DNA POLYMERASE

V93R MUTANT: [XXX] $\underline{NNN} = AGA$, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 27)

V93E MUTANT: [XXX] $\underline{NNN} = GAA$, GAG (ALL CODONS FOR GLUTAMIC ACID) $\underline{(SEQ)}$ ID NO: 28)

```
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT[XXX]MNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGTG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
```

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PFU DNA POLYMERASE
G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 29)
V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT [XXX] NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
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PFU DNA POLYMERASE

D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)

ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

V93R MUTANT: [XXX] $\underline{NNN} = AGA$, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 31)

V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEO ID NO: 32)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120

```
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT [XXX] NNNC CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGTG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACA [CC N] GGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328
KOD DNA POLYMERASE
V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 33)
V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ID NO: 34)
ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180
ACGGTTGTAA CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240
GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGAC[XXX]NNNC CAGCGATAAG GGACAAGATA 300
CGAGAGCATC CAGCAGTTAT TGACATCTAC GAGTACGACA TACCCTTCGC CAAGCGCTAC 360
CTCATAGACA AGGGATTAGT GCCAATGGAA GGCGACGAGG AGCTGAAAAT GCTCGCCTTC 420
GACATTGAAA CTCTCTACCA TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CCTTATGATA 480
AGCTACGCCG ACGAGGAAGG GGCCAGGGTG ATAACTTGGA AGAACGTGGA TCTCCCCTAC 540
GTTGACGTCG TCTCGACGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT TGTGAAGGAG 600
AAAGACCCGG ACGTTCTCAT AACCTACAAC GGCGACAACT TCGACTTCGC CTATCTGAAA 660
AAGCGCTGTG AAAAGCTCGG AATAAACTTC GCCCTCGGAA GGGATGGAAG CGAGCCGAAG 720
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ATTCAGAGGA TGGGCGACAG GTTTGCCGTC GAAGTGAAGG GACGGATACA CTTCGATCTC 780

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TATCCTGTGA TAAGACGGAC GATAAACCTG CCCACATACA CGCTTGAGGC CGTTTATGAA 840
GCCGTCTTCG GTCAGCCGAA GGAGAAGGTT TACGCTGAGG AAATAACCAC AGCCTGGGAA 900
ACCGGCGAGA ACCTTGAGAG AGTCGCCCGC TACTCGATGG AAGATGCGAA GGTCACATAC 960
GAGCTTGGGA AGGAGTTCCT TCCGATGGAG GCCCAGCTTT CTCGCTTAAT CGGCCAGTCC 1020
CTCTGGGACG TCTCCCGCTC CAGCACTGGC AACCTCGTTG AGTGGTTCCT CCTCAGGAAG 1080
GCCTATGAGA GGAATGAGCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT GGCCAGAAGA 1140
CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG GGAGAACATA 1200
GTGTACCTAG ATTTTAGATC CCTGTACCCC TCAATCATCA TCACCCACAA CGTCTCGCCG 1260
GATACGCTCA ACAGAGAAGG ATGCAAGGAA TATGACGTTG CCCCACAGGT CGGCCACCGC 1320
CAGAAGATAA AGAAGAAGAT GAAGGCCACG ATTGACCCGA TCGAGAGGAA GCTCCTCGAT 1440
TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT ACGGTTACTA CGGCTATGCA 1500
AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA CGGCCTGGGG AAGGGAGTAC 1560
ATAACGATGA CCATCAAGGA GATAGAGGAA AAGTACGGCT TTAAGGTAAT CTACAGCGAC 1620
ACCGACGGAT TTTTTGCCAC AATACCTGGA GCCGATGCTG AAACCGTCAA AAAGAAGGCT 1680
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GGCTTCTACA AACGCGGCTT CTTCGTCACG AAGAAGAAGT ATGCGGTGAT AGACGAGGAA 1800
GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA 1860
GAGACGCAGG CGAGGGTTCT TGAAGCTTTG CTAAAGGACG GTGACGTCGA GAAGGCCGTG 1920
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GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG TCCCCACGTT 2040
GCCGTTGCCA AGAGGTTGGC CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC 2100
TACATCGTGC TCAAGGGCTC TGGGAGGATA GGCGACAGGG CGATACCGTT CGACGAGTTC 2160
GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC 2220
GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG 2280
AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CTTGA 2325
Vent DNA POLYMERASE
V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 35)
V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ID NO: 36)
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60
AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120
CTTCTCAAAG ATGACTCCGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA 180
AAAACTGTGA GAGTGCTCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG AAGGGAAGTT 240
GAAGTCTGGA AGCTCATTTT CGAGCATCCC CAAGAC [XXX] NNNC CAGCTATGCG GGGCAAAATA 300
AGGGAACATC CAGCTGTGGT TGACATTTAC GAATATGACA TACCCTTTGC CAAGCGTTAT 360
CTCATAGACA AGGGCTTGAT TCCCATGGAG GGAGACGAGG AGCTTAAGCT CCTTGCCTTT 420
GATATTGAAA CGTTTTATCA TGAGGGAGAT GAATTTGGAA AGGGCGAGAT AATAATGATT 480
AGTTATGCCG ATGAAGAAGA GGCCAGAGTA ATCACATGGA AAAATATCGA TTTGCCGTAT 540
GTCGATGTTG TGTCCAATGA AAGAGAAATG ATAAAGCGTT TTGTTCAAGT TGTTAAAGAA 600
AAAGACCCCG ATGTGATAAT AACTTACAAT GGGGACAATT TTGATTTGCC GTATCTCATA 660
AAACGGCAG AAAAGCTGGG AGTTCGGCTT GTCTTAGGAA GGGACAAAGA ACATCCCGAA 720
CCCAAGATTC AGAGGATGGG TGATAGTTTT GCTGTGGAAA TCAAGGGTAG AATCCACTTT 780
GATCTTTTCC CAGTTGTGCG AAGGACGATA AACCTCCCAA CGTATACGCT TGAGGCAGTT 840
TATGAAGCAG TTTTAGGAAA AACCAAAAGC AAATTAGGAG CAGAGGAAAT TGCCGCTATA 900
TGGGAAACAG AAGAAAGCAT GAAAAAACTA GCCCAGTACT CAATGGAAGA TGCTAGGGCA 960
ACGTATGAGC TCGGGAAGGA ATTCTTCCCC ATGGAAGCTG AGCTGGCAAA GCTGATAGGT 1020
CAAAGTGTAT GGGACGTCTC GAGATCAAGC ACCGGCAACC TCGTGGAGTG GTATCTTTTA 1080
AGGGTGGCAT ACGCGAGGAA TGAACTTGCA CCGAACAAAC CTGATGAGGA AGAGTATAAA 1140
CGGCGCTTAA GAACAACTTA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA AGGTTTGTGG 1200
GAAAATATCA TTTATTTGGA TTTCCGCAGT CTGTACCCTT CAATAATAGT TACTCACAAC 1260
GTATCCCCAG ATACCCTTGA AAAAGAGGGC TGTAAGAATT ACGATGTTGC TCCGATAGTA 1320
GGATATAGGT TCTGCAAGGA CTTTCCGGGC TTTATTCCCT CCATACTCGG GGACTTAATT 1380
GCAATGAGGC AAGATATAAA GAAGAAAATG AAATCCACAA TTGACCCGAT CGAAAAGAAA 1440
ATGCTCGATT ATAGGCAAAG GGCTATTAAA TTGCTTGCAA ACAGCTATTA CGGCTATATG 1500
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GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CGCATGGGGG 1560
AGACACTACA TAGAGATGAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAGGTTCTT 1620
TATGCGGACA CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA 1680
AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT GCTTGAGCTT 1740
GAGTATGAGG GCTTTTACTT GAGAGGATTC TTTGTTACAA AAAAGCGCTA TGCAGTCATA 1800
GATGAAGAGG GCAGGATAAC AACAAGGGGC TTGGAAGTAG TAAGGAGAGA TTGGAGTGAG 1860
ATAGCTAAGG AGACTCAGGC AAAGGTTTTA GAGGCTATAC TTAAAGAGGG AAGTGTTGAA 1920
AAAGCTGTAG AAGTTGTTAG AGATGTTGTA GAGAAAATAG CAAAATACAG GGTTCCACTT 1980
GAAAAGCTTG TTATCCATGA GCAGATTACC AGGGATTTAA AGGACTACAA AGCCATTGGC 2040
CCTCATGTCG CGATAGCAAA AAGACTTGCC GCAAGAGGGA TAAAAGTGAA ACCGGGCACA 2100
ATAATAAGCT ATATCGTTCT CAAAGGGAGC GGAAAGATAA GCGATAGGGT AATTTTACTT 2160
ACAGAATACG ATCCTAGAAA ACACAAGTAC GATCCGGACT ACTACATAGA AAACCAAGTT 2220
TTGCCGGCAG TACTTAGGAT ACTCGAAGCG TTTGGATACA GAAAGGAGGA TTTAAGGTAT 2280
CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA GGTAG 2325
Deep Vent
V93R MUTANT: [XXX]
                    NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE
CODONS FOR ARGININE) (SEQ ID NO: 37)
V93E MUTANT: [XXX] MNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ
ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG
                                                                     60
AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT
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CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG
                                                                    180
AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT
                                                                    240
GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGAC[XXX]NNNC CCGCAATAAG GGATAAGATA
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AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC
CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT
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GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA
                                                                    480
AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC
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GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG
                                                                    600
AAAGATCCCG ATGTTATAAT TACCTACAAC GGCGATTCTT TCGACCTTCC CTATCTAGTT
                                                                    660
AAGAGGGCCG AAAAGCTCGG GATAAAGCTA CCCCTGGGAA GGGACGGTAG TGAGCCAAAG
                                                                    720
ATGCAGAGGC TTGGGGATAT GACAGCGGTG GAGATAAAGG GAAGGATACA CTTTGACCTC
TACCACGTGA TTAGGAGAAC GATAAACCTC CCAACATACA CCCTCGAGGC AGTTTATGAG
                                                                    840
GCAATCTTCG GAAAGCCAAA GGAGAAAGTT TACGCTCACG AGATAGCTGA GGCCTGGGAG
                                                                    900
ACTGGAAAGG GACTGGAGAG AGTTGCAAAG TATTCAATGG AGGATGCAAA GGTAACGTAC
                                                                    960
GAGCTCGGTA GGGAGTTCTT CCCAATGGAG GCCCAGCTTT CAAGGTTAGT CGGCCAGCCC 1020
CTGTGGGATG TTTCTAGGTC TTCAACTGGC AACTTGGTGG AGTGGTACCT CCTCAGGAAG 1080
GCCTACGAGA GGAATGAATT GGCTCCAAAC AAGCCGGATG AGAGGAGTA CGAGAGAAGG
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CTAAGGGAGA GCTACGCTGG GGGATACGTT AAGGAGCCGG AGAAAGGGCT CTGGGAGGGG
                                                                   1200
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TTAGTTTCCC TAGATTTCAG GAGCCTGTAC CCCTCGATAA TAATCACCCA TAACGTCTCA 1260 CCGGATACGC TGAACAGGGA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC

GCAAAAGCCC GTTGGTACTG TAAGGAGTGC GCAGAGAGCG TTACGGCCTG GGGGAGGGAA 1560 TATATAGAGT TCGTAAGGAA GGAACTGGAG GAAAAGTTCG GGTTCAAAGT CTTATACATA 1620 GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA 1680 GCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC 1740 GAGGGCTTCT ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT GATAGATGAG 1800 GAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG CGAAATAGCC 1860 AAAGAAACCC AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGAGGCA 1920 GTAAAGATAG TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG 1980 CTAGTTATTT ACGAGCAGAT CACGAGGCCC CTTCACGAGT ACAAGGCTAT AGGTCCGCAC 2040 GTTGCCGTGG CAAAAAGGTT AGCCGCTAGA GGAGTAAAGG TGAGGCCTGG CATGGTGATA 2100 GGGTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG

TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT 2220

AAGTTCTGCA AGGACTTCCC GGGGTTTATC CCCAGCCTGC TCAAGAGGTT ATTGGATGAA

AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC CAATCGAGAA GAAGATGCTT

GATTACAGGC AACGGGCAAT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC

1320

1380

1440

1500

2160

JDF-3

V93R MUTANT: [XXX] NNN = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) (SEQ ID NO: 39) V93E MUTANT: [XXX] NNN = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) (SEQ

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGGACGGCGAGTTCA GGATTGAATACGACCGCGAGTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAA GATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGGCAGGTCT GTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGAC [XXX] MNNCCGGCAATCCGCGACAAAATAAGGAAGCACCC CGCGGTCATCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTTACCTCATAGACAAGGGCCTAATCCCGATGGAA GGTGAGGAAGAGCTTAAACTCATGTCCTTCGACATCGACGACGCTCTACCACGAGGGAGAAGAGTTTGGAACCGGGCCGA TGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATAC GGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCC AGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAG AAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGG ACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCT GCTCCCAACAAGCCCGACGAGGAGGGGGGCTGGCGAGGAGGAGGAGGGGGGGCTACGTCAAGGAGCCGGAGC GGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCCTTCAATCATAATCACCCACAACGTCTCGCC ${\tt AGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCG} \overline{{\tt AGGTCACAAGGTTCTGCAAGGACTTCCCC}}$ GGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACC CGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCCATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA TGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATC AGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGG ACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTCGAACTCGA ATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACC ACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGGTAACCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATAC TCAGGCACGTGACGTTGAAGAGGCCGTCAGAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCC GGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCG AAqcGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGA TAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCA GGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAG GTCGGGCTTGGCGCTGAAGCCGAAGGGGAAGAAGAAGTGA

MARKED UP VERSION OF AMENDED FIGURE 13B

Please replace Figure 13B with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 13B.

Figure 13B

>Pfu V93R (SEQ ID NO:41)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS //

>Pfu V93E (SEQ ID NO:42)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/G387P (SEQ ID NO:43)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
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KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93R/D141A/E143A(SEQ ID NO:44)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRDW

SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL NIKKS

>Pfu V93E/G387P(SEQ ID NO:45)

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KPITVWKLYLEHPQDEPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TPGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>Pfu V93E/D141A/E143A(SEQ ID NO:46)

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KPITVWKLYLEHPQDRPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFAIATLYHEGEEFGK
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IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESY
TGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVK
IKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWL
NIKKS

>DEEP VENT V93R (SEQ ID NO:47)

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GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAEYYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWL
NIKKK

>DEEP VENT V93E (SEQ ID NO:48)

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GPIIMISYADEEEAKVITWKKIDLPYVEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPLHEYKAIGPHVAVAKRLAARGVK
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NIKKK

Marked-Up Version

>TGO V93R (SEQ ID NO:49)

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GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>TGO V93E (SEQ ID NO:50)

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLG
RPIEVWKLYFTHPQDEPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQK
VKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYA
DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD V93R(SEQ ID NO:51)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDRPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>KOD V93E(SEQ ID NO:52)

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLYFTHPQDEPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITPAWETGENLERV
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKI

RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLSAWLK PKGT

>VENT V93R(SEQ ID NO:53)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDRPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>VENT V93E(SEQ ID NO:54)

MILDTDYITKDGKPIIRIFKKENGEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDEPAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIMISYADEEEARVITWKNIDLPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDLPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIHFDLFPVVRRTINLPTYTLEAVYEAVLGKTKSKLGAEEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSSTGNLVEWYLLRVAYARNELAPNKPDEEEYKRRLRT
TYLGGYVKEPEKGLWENIIYLDFRSLYPSIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSILGDLIAM
RQDIKKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIHEQITRDLKDYKAIGPHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYYIENQVLPAVLRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 V93R(SEQ ID NO:55)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR SVEVWVLYFTHPQDRPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

>JDF-3 V93E(SEQ ID NO:56)

MILDVDYITENGKPVIRVFKKENGEFRIEYDREFEPYFYALLRDDSAIEEIKKITAERHGRVVKVKRAEKVKKKFLGR SVEVWVLYFTHPQDEPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGTGP ILMISYADESEARVITWKKIDLPYVEVVSTEKEMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGR DGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIATAWETGEGLERVARYS MEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGGYAGGYVK EPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFCKDFPGFIPSLLGNLLEERQKIKRKMK ATLDPLEKNLLDYRQRAIKILANSYYGYYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA TIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQA RVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIHEQITRELKDYKATGPHVAIAKRLAARGVKIRPGTVISYI VLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKGKKK

MARKED UP VERSION OF AMENDED FIGURE 14

Please replace Figure 14 with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 14.

Figure 14

	= A0							CGT (INO .	ACID	SEQU	JENCI	3: S	ВQ	ID	NO:	58)
		AA, C			3: SI	3O II	ONO:	: 59;	AM]	INO .	ACID	SEQU	JENCI	3: S	EQ	ID	NO:	60)
5' atq	atc	ctc	gat	aca	gac	tac	ata	act	gag	gat	gga	aag	ccc	qtc	at	.c		48
Met	Ile	Leu	Asp	Thr	Asp	Tyr	Ile	Thr	Glu	Asp	Gly	Lys	Pro	Val	ıı	.e		
1				5					10					15				
agg	atc	ttc	aag	aag	gag	aac	ggc	gag	ttc	aaa	ata	gac	tac	gac	ag	ja		96
Arg	Ile	Phe	Lys	Lys	Glu	Asn	Gly	Glu	Phe	Lys	Ile	Asp	Tyr	Asp	Ar	g		
			20					25					30					
aac	ttt	gag	cca	tac	atc	tac	gcg	ctc	ttg	aag	gac	gac	tct	gcg	at	t		144
Asn	Phe	Glu	Pro	Tyr	Ile	Tyr	Ala	Leu	Leu	Lys	Asp	Asp	Ser	Ala	11	.e		
		35					40					45						
gag	gac	gtc	aag	aag	ata	act	gcc	gag	agg	cac	ggc	act	acc	gtt	ag	19		192
Glu	Asp	Val	Lys	Lys	Ile	Thr	Ala	Glu	Arg	His	Gly	Thr	Thr	Val	Ar	g		
	50					55					60							
_	_		_				_	_	_		cta			_				240
	Val	Arg	Ala	Glu	_	Val	Lys	Lys	Lys	Phe	Leu	Gly	Arg	Pro				
65					70					75					80)		

gag	gtc	tgg	aag	ctc	tac	ttc	act	cac	CCC	cag	gac	nnn	ccc	gca	atc	288
Glu	Val	Trp	Lys	Leu	Tyr	Phe	Thr	His	Pro	Gln	Asp	Xaa	Pro	Ala	Ile	
				85					90					95		
agg	gac	aag	ata	aag	gag	cat	cct	gcc	gtt	gtg	gac	atc	tac	gag	tac	336
Arg	Asp	Lys	Ile	Lys	Glu	His	Pro	Ala	Val	Val	Asp	Ile	Tyr	Glu	Tyr	
			100					105					110			
gac	atc	ccc	ttc	gcg	aag	cgc	tac	ctc	ata	gac	aaa	ggc	tta	atc	ccg	384
Asp	Ile	Pro	Phe	Ala	Lys	Arg	Tyr	Leu	Ile	Asp	Lys	Gly	Leu	Ile	Pro	
		115					120					125				
atg	gag	ggc	gac	gag	gaa	ctt	aag	atg	ctc	gcc	ttc	gac	atc	gag	acg	432
Met	Glu	Gly	Asp	Glu	Glu	Leu	Lys	Met	Leu	Ala	Phe	Asp	Ile	Glu	Thr	
	130					135					140					
ctc	tat	cac	gag	ggc	gag	gag	ttc	gcc	gaa	ggg	cct	atc	ctg	atg	ata	480
Leu	Tyr	His	Glu	Gly	Glu	Glu	Phe	Ala	Glu	Gly	Pro	Ile	Leu	Met	Ile	
145					150					155					160	
				•												
agc	tac	gcc	gac	gag	gaa	ggg	gcg	cgc	gtt	att	acc	tgg	aag	aat	atc	528
Ser	Tyr	Ala	Asp	Glu	Glu	Gly	Ala	Arg	Val	Ile	Thr	Trp	Lys	Asn	Ile	
				165					170					175		
gac	ctt	ccc	tat	gtc	gac	gtc	gtt	tcc	acc	gag	aag	gag	atg	ata	aag	576
Asp	Leu	Pro	Tyr	Val	Asp	Val	Val	Ser	Thr	Glu	Lys	Glu	Met	Ile	Lys	
			180					185					190			

cgc	ttc	ctc	aag	gtc	gtc	aag	gaa	aag	gat	ccc	gac	gtc	ctc	ata	acc	624
Arg	Phe	Leu	Lys	Val	Val	Lys	Glu	Lys	Asp	Pro	Asp	Val	Leu	Ile	Thr	
		195					200					205				
tac	aac	ggc	gac	aac	ttc	gac	ttc	gcc	tac	ctc	aag	aag	cgc	tcc	gag	672
Tyr	Asn	Gly	Asp	Asn	Phe	Asp	Phe	Ala	Tyr	Leu	Lys	Lys	Arg	Ser	Glu	
	210					215					220					
			_										gag			720
Lys	Leu	Gly	Val	Lys	Phe	Ile	Leu	Gly	Arg	Glu	Gly	Ser	Glu	Pro	Lys	
225					230					235					240	
		_											gga			768
Ile	Gln	Arg	Met		Asp	Arg	Phe	Ala		Glu	Val	Lys	Gly		Ile	
				245					250					255		
																016
													ctc			816
HIS	Pne	Asp		Tyr	Pro	vai	11e		Arg	inr	iie	ASN	Leu	PIO	inr	
			260					265					270			
tac	200	ctt	asa	aca	ata	tat	gaa	acc	atc	+++	gga	cag	ccg	aad	gag	864
			_	_	_		_	_					Pro			331
-1-	1111	275	014			-1-	280				1	285		-,-		
aaq	qtc	tac	qct	gag	qaq	ata	gca	caq	gcc	tga	gaa	acq	ggc	gaq	gga	912
	_		_										Gly			
•	290	•				295				*	300		•		-	

tta	gaa	agg	gtg	gcc	cgc	tac	tcg	atg	gag	gac	gca	aag	gta	acc	tat		960
Leu	Glu	Arg	Val	Ala	Arg	Tyr	Ser	Met	Glu	Asp	Ala	Lys	Val	Thr	Tyr		
305					310					315					320		
gaa	ctc	gga	aaa	gag	ttc	ttc	cct	atg	gaa	gcc	cag	ctc	tcg	cgc	ctc	1	.008
Glu	Leu	Gly	Lys	Glu	Phe	Phe	Pro	Met	Glu	Ala	Gln	Leu	Ser	Arg	Leu		
				325					330					335			
gta	ggc	cag	agc	ctc	tgg	gat	gta	tct	cgc	tcg	agt	acc	gga	aac	ctc	1	.056
Val	Gly	Gln	Ser	Leu	Trp	Asp	Val	Ser	Arg	Ser	Ser	Thr	Gly	Asn	Leu		
			340					345					350				
gtc	gag	tgg	ttt	ttg	ctg	agg	aag	gcc	tac	gag	agg	aat	gaa	ctt	gca	1	104
Val	Glu	Trp	Phe	Leu	Leu	Arg	Lys	Ala	Tyr	Glu	Arg	Asn	Glu	Leu	Ala		
		355					360					365					
сса	aac	aag	ccg	gac	gag	agg	gag	ctg	gca	aga	aga	agg	gag	agc	tac	1	152
Pro	Asn	Lys	Pro	Asp	Glu	Arg	Glu	Leu	Ala	Arg	Arg	Arg	Glu	Ser	Tyr		
	370					375					380						
gcg	ggt	gga	tac	gtc	aag	gag	ccc	gaa	agg	gga	ctg	tgg	gag	aac	atc	1	200
Ala	Gly	Gly	Tyr	Val	Lys	Glu	Pro	Glu	Arg	Gly	Leu	Trp	Glu	Asn	Ile		
385					390					395					400		
gtg	tat	ctg	gac	ttc	cgc	tcc	ctg	tat	cct	tcg	ata	ata	atc	acc	cat	1	L248
Val	Tyr	Leu	Asp	Phe	Arg	Ser	Leu	Tyr	Pro	Ser	Ile	Ile	Ile	Thr	His		
				405					410					415			

aac	gtc	tcc	cct	gat	aca	ctc	aac	agg	gag	ggt	tgt	gag	gag	tac	gac	1296
Asn	Val	Ser	Pro	Asp	Thr	Leu	Asn	Arg	Glu	Gly	Cys	Glu	Glu	Tyr	Asp	
			420					425					430			
gtg	gct	cct	cag	gta	ggc	cat	aag	ttc	tgc	aag	gac	ttc	ccc	ggc	ttc	1344
Val	Ala	Pro	Gln	Val	Gly	His	Lys	Phe	Cys	Lys	Asp	Phe	Pro	Gly	Phe	
		435					440					445				
atc	cca	agc	ctc	ctc	gga	gac	ctc	ttg	gag	gag	aga	cag	aag	gta	aag	1392
Ile	Pro	Ser	Leu	Leu	Gly	Asp	Leu	Leu	Glu	Glu	Arg	Gln	Lys	Val	Lys	
	450					455					460					
aad	aad	ata	aad	acc	act	ata	gac	cca	atc	gag	aag	aaa	ctc	ctc	gat	1440
_	_										_			Leu		1110
_	цуѕ	Mec	пур	AIA		116	Asp	PIO	116		пуѕ	пуъ	пеп	ьeu	_	
465					470					475					480	
														ggt		1488
Tyr	Arg	Gln	Arg	Ala	Ile	Lys	Ile	Leu	Ala	Asn	Ser	Phe	Tyr	Gly	Tyr	
				485					490					495		
tac	ggc	tat	gca	aag	gcc	cgc	tgg	tac	tgc	aag	gag	tgc	gcc	gag	agc	1536
Tyr	Gly	Tyr	Ala	Lys	Ala	Arg	Trp	Tyr	Cys	Lys	Glu	Суѕ	Ala	Glu	Ser	
			500					505					510			
gtt	acc	gct	tgg	ggc	agg	cag	tac	atc	gag	acc	acg	ata	agg	gaa	ata	1584
Val	Thr	Ala	Trp	Gly	Arg	Gln	Tyr	Ile	Glu	Thr	Thr	Ile	Arg	Glu	Ile	
		515					520					525				

gag	gag	aaa	ttt	ggc	ttt	aaa	gtc	ctc	tac	gcg	gac	aca	gat	gga	ttt	1632
Glu	Glu	Lys	Phe	Gly	Phe	Lys	Val	Leu	Tyr	Ala	Asp	Thr	Asp	Gly	Phe	
	530					535					540					
ttc	gca	aca	ata	cct	gga	gcg	gac	gcc	gaa	acc	gtc	aaa	aag	aag	gca	1680
Phe	Ala	Thr	Ile	Pro	Gly	Ala	Asp	Ala	Glu	Thr	Val	Lys	Lys	Lys	Ala	
545					550					555					560	
aag	gag	ttc	ctg	gac	tac	atc	aac	gcc	aaa	ctg	ccc	ggc	ctg	ctc	gaa	1728
Lys	Glu	Phe	Leu	Asp	Tyr	Ile	Asn	Ala	Lys	Leu	Pro	Gly	Leu	Leu	Glu	
				565					570					575		
ctc	gaa	tac	gag	ggc	ttc	tac	aag	cgc	ggc	ttc	ttc	gtg	acg	aag	aag	1776
Leu	Glu	Tyr	Glu	Gly	Phe	Tyr	Гуs	Arg	Gly	Phe	Phe	Val	Thr	Lys	Lys	
			580					585					590			
aag	tac	gcg	gtt	ata	gac	gag	gag	gac	aag	ata	acg	acg	cgc	a aa	ctt	1824
Lys	Tyr	Ala	Val	Ile	Asp	Glu	Glu	Asp	Lys	Ile	Thr	Thr	Arg	Gly	Leu	
		595					600					605				
gaa	ata	gtt	agg	cgt	gac	tgg	agc	gag	ata	gcg	aag	gag	acg	cag	gcg	1872
Glu	Ile	Val	Arg	Arg	Asp	Trp	Ser	Glu	Ile	Ala	Lys	Glu	Thr	Gln	Ala	
	610					615					620					
agg	gtt	ctt	gag	gcg	ata	cta	aag	cac	ggt	gac	gtt	gaa	gaa	gcg	gta	1920
Arg	Val	Leu	Glu	Ala	Ile	Leu	Lys	His	Gly	Asp	Val	Glu	Glu	Ala	Val	
625					630					635					640	

agg	att	gtc	aaa	gag	gtt	acg	gag	aag	ctg	agc	aag	tac	gag	gtt	cca	1968
Arg	Ile	Val	Lys	Glu	Val	Thr	Glu	Lys	Leu	Ser	Lys	Tyr	Glu	Val	Pro	
				645					650					655		
ccg	gag	aag	ctg	gtc	atc	tac	gag	cag	ata	acc	cgc	gac	ctg	aag	gac	2016
Pro	Glu	Lys	Leu	Val	Ile	Tyr	Glu	Gln	Ile	Thr	Arg	Asp	Leu	Lys	Asp	
			660					665					670			
tac	aag	gcc	acc	999	ccg	cat	gtg	gct	gtt	gca	aaa	cgc	ctc	gcc	gca	2064
Tyr	Lys	Ala	Thr	Gly	Pro	His	Val	Ala	Val	Ala	Lys	Arg	Leu	Ala	Ala	
		675					680					685				
agg	999	ata	aaa	atc	cgg	ccc	gga	acg	gtc	ata	agc	tac	atc	gtg	ctc	2112
Arg	Gly	Ile	Lys	Ile	Arg	Pro	Gly	Thr	Val	Ile	Ser	Tyr	Ile	Val	Leu	
	690					695					700					
aaa	ggc	tcg	gga	agg	att	333	gac	agg	gct	ata	ccc	ttt	gac	gaa	ttt	2160
Lys	Gly	Ser	Gly	Arg	Ile	Gly	Asp	Arg	Ala	Ile	Pro	Phe	Asp	Glu	Phe	
705					710					715					720	
gac	ccg	gca	aag	cac	aag	tac	gat	gca	gaa	tac	tac	atc	gag	aac	cag	2208
Asp	Pro	Ala	Lys	His	Lys	Tyr	Asp	Ala	Glu	Tyr	Tyr	Ile	Glu	Asn	Gln	
				725					730					735		
_					gag					_						2256
Val	Leu	Pro		Val	Glu	Arg	Ile		Arg	Ala	Phe	Gly	_	Arg	Lys	
			740					745					750			

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg 2304
Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp
755 760 765

cta aaa cct aag aca tga

2322

Leu Lys Pro Lys Thr

Figure 17A

Pyrococcus	CCUB	fur	furiosus gene	gen	te fc	for ar	archaeal	al h	histone (HMf-like) [Fig.17-A]	ne (HME-	like	.) [Fi	g.17	-A]			
(ACCESSION No: AB013081)	SION	No:	AB01	3081														
Nucleotide	tide		sequence	SE	(SEQ ID	NO:	NO: 63)	,										
Amino	acid		sequence	(SEQ	CI O	NO:	64)	; II										
Σ				J	д	н	Æ	Д	>	Q	ድ	ч	н	D.	×	Ø	ტ	ñ
ATG	ATG	GGA	GAA	TTA	CCA	ATT	gcc	CCA	GTT	GAC	AGA	CTT	ATA	AGA	AAG	GCT	GGT	2
A				တ	ы	ø	Ą	Ø	×	>	ц	ø	ы	н	J	ជ	臼	ä
GCT	CAG	AGA	GTT	AGC	GAG	CAA	GCA	GCT	AAG	GTA	CLL	GCA	GAG	CAC	CTT	GAG	GAA	101
×				н	Ø	×	×	ø	>	Д	ы	ø	×	Ħ	Ø	დ	ፚ	Š
AAA	GCT	ATT	GAG	ATC	GCA	AAA	AAG	GCA	GTA	GAT	CTT	GCA	AAG	CAC	GCA	GGT	AGA	16
×				>		Д	н	×		Ø	н	×	ഗ	*				9
AAG	ACC	GTT	AAG	GIC	GAA	GAC	ATT	AAG	CIC	GCA	ATT	AAG	AGC	TGA				20.

Figure 17B

(HMf-like)-Taq DNA polymerase fusion protein [Fig.17-B]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 64) // Amino acid sequence (SEQ ID NO: 66)

	54	36			162	69	
)	GGT	臼	GAA	œ	AGA		
;	GCT	团	GAG	ტ	GGT		
;	AAG	ч		Ø	GCA		
4	AGA	Ħ	CAC	Ħ	CAC		
1	ATA	凶	GAG	×	AAG	ഗ	AGC
7	CTT	Ø	GCA	Ø	GCA	×	
4	AGA	ц	CII	ы	CTT	н	ATT
3	GAC	>	GTA	Д	GAT	Ø	GCA
>	GTT	×	AAG	>	GTA	ы	CTC
4	CCA	Ą	GCT	Ø	GCA	×	AAG
¢	325	Ą	GCA	×	AAG	Н	ATT
4	ATT	ø	CAA	×	AAA		
4	CCA	田	GAG	Ø	GCA	VED	GAA
7	TTA	ß	AGC	н	ATC	>	GTC
1	GAA	>	GTT	ы	GAG	×	AAG
כ	GGA	ഷ	AGA	н	ATT	>	GTT
Ξ	ATG	ø	CAG	Ø	GCT	H	ACC
Ξ	ATG	Ø	GCT	×	AAA	K	AAG

V GTG L F E P K G R V L L CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG CCC $_{
m CTG}$ M ATG V T S G GTC ACT AGT GGG R T F H A L K G L T T CGC ACC TTC CAC GCC CTG AAG GGC CTC ACC ACC Y TAC GCC L CTG CAC H CAC ၁၉ D GAC Y G F A K S L L K
TAC GGC TTC GCC AAG AGC CTC CTC AAG [X]<u>∨</u> [0]<u>G</u>TC 1 A GCG CAG V GTG P E ი მვვ R CGG s AGC

မှ ငြင်င A GCC V I V V F D A K GTG ATC GTG GTC TTT GAC GCC AAG A GCG DGAC ი გვვ D GAC E GAG K AAG CIC A

G P T ACG CCC gcc Cc GGG PA ဗ ဥ္ဌ GCG Y K TAC AAG (ი მვვ ი ცვ Y TAC gcc Gcc E CAC GGC B F TTC s TCC

စ ဗ္ဗ r CTG CIC V D GTG GAC I K E L ATC AAG GAG CTG CIC A GCC CTC CAA R CGG CCC F TTT D GAC GAG

L s AGC GCC CTG V GTC Y E A D D TAC GAG GCG GAC GAC ဗဗ P V GTC L E CTC GAG (GGC A GCG CTG

K AAA D GAC G Y E V R I L T A GGC TAC GAG GTC CGC ATC CTC ACC GCC K A E K E AAG GCG GAA AAG GAG A K GCC AAG A

Y TAC . GGG E GAG CCC CAC CIC V GTC CAC I ATC R CGC DGAC S LCTT L CAG Y TAC CTT GAC W TGG CAG GAC CCC Д R AGG Γ ဗ္ဗင္ဗ Y AAG 노 GAA 回 TGG. L WA GCC P T ACC I ATC L

K AAG V GTC ი მვი CCC LCTT N AAC DGAC s TCC GAG DGAC ა ე T LCTG A GCC R Y TAC GAC A GCC CIG GAG E r CTG CTT K AAG R AGG T A A ACG GCG P E K GAG AAG 1 ATC D 3AC ₹ ÇC မှ ညီ V GTG K AAG A GC r CTG D GAC ĭĞĞ s Icc r CTC K AAG LCTG DGAT D 3AC M ATG H A GCC

r F R AGG E R CGG GAC မှ ည E R CGG R AGG AAA AAA A GCC F DGAC V GTG E r CTG မ ည L CTG r FT ဗ္ဗဋ္ဌ F E H CTC LCTC s AGC ය ශීරී F TTT E LCTT R AGG E L FTTT A GCC R AGG

A GCC ပ္ပဋ္ဌ E GAA P P မှ W TGG P A GCC E E L ₽ GCC K AAG P S AGC E GAA L CTG

A GCC r CTG CIT D GAT A GCC W TGG M ATG r CCC E K AAG GGC R S CTT V GTG F TTT ဗ္ဗဋ္ဌ V GTG F

A GCC A A Y TAT PCCT GAG CCC A GCC R GGG CAC V GTC CGG 9 9 ი მვვ R AGG A G A GCC A GCC LCTG

r CTG V GTT S AGC CTG DGAC K AAA A GCC r CTC CTT ი მვვ CGG A GCG E GAG K AAG r CTG DGAC R AGG CTC

A CTC LCTC M ATG က္ရင္သ D GAC DGAC ၁၁၅ CCC P r CTC g GGC LCTT ဗဗ GAA R AGG $_{\rm CTG}^{\rm L}$ gg A g 3GC Y TAC အ င်င်င ය දු A V GTG ი მვვ E က် ACC. T ACC N AAC s TCC CCT D CTG r CTC Y

F L R AGG E s TCC L A GCC A GCC ස පු E G GGG A GCG E E GAG T ACG W E ი მვვ

R GG Y CTT W TGG LCTT CHC R AGG E E ဗ္ဗဗ္ဗ E L R AGG ი ცვვ W L N AAC A S V GTG G G G T ACG 3CC E M ATG HCAC မွ ဗ L V GTC A GCT S ICC L က်င္ပင္ပင္ R AGG E V GTG E

EGAG E GAG A GCC V GTG E GAG r CTG s TCC $_{\mathrm{TTG}}$ A r Agg CIC Y TAT gcc Gcc GTG > D GAC CTG Ы က္က ပိုင္ပဲ

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TAC
                    V
GTG
                                                  ဗ္ဗ
                    R
CGG
                                                   CAG
AAG GTG CGG GCC TGG ATT GAG AAG ACC CTG GAG GAG GGC AGG AGG CGG GGG
                                                  F N M P V
TTC AAC ATG CCC GTC
                   L E A
CTA GAG GCC
                   L F G R R R Y V P D CTC TTC GGC CGC CGC TAC GTG CCA GAC
                                                  A A E R M A
GCG GCC GAG CGC ATG GCC
                                                  R E
CGG GAG (
                    T
ACC
                                                   V
GTG
                   V E
GTG GAG 1
                                                   K S
AAG AGC
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E GAG r CTG P R CCC AGG F D L M K L A M V K L GAC CTC ATG AAG CTC GCC GCC T A ACC GCC

A GCC V L E GTC CTC GAG r CTG D E GAC GAG (A R M L L Q V H GCC AGG ATG CTC CTT CAG GTC CAC ი მვვ E M GAA ATG

ი გვე GAG E R A E A V A R L A K E V M GAG AGG GGG GAG GCC CGC CGG CTG GCC AAG GAG GTC ATG P K CCA AAA

₩ TGG D GAC V Y P L A V P L E V E V G I G E GTG TAT CCC CTG GCG CTG GAG GTG GGG ATA GGG GAG

CAT H L S A K E G I D G R G G G H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT

H H * CAT CAT TAA

Figure 17C

Taq DNA polymerase- (HMf-like) fusion protein [Fig.17-C]

Amino acid sequence (SEQ ID NO: 66) / Amino acid sequence (SEQ ID NO: 64) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 63)

G G G //

V GTG r CTG V T S G M L P L F E P K G R V L GTC ACT AGT GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC

Marked-Up Verison

K AAG CTC A K S L GCC AAG AGC CTC Y G F TAC GGC TTC [X]<u>V</u> [0]<u>G</u>TC A GCG CAG V GTG P CCG E g ggg r G နှင့် နိုင္ပင

P CCC A GCC K AAG A GCC D GAC F TTT V I V V GTG ATC A GCG DGAC ი მვვ D GAC E GAG K AAG L A 3CC P P T ACG P CCC A GCC R GGG ggc A GCG K AAG Y TAC ი მვვ ი მმ Y TAC A GCC EGAG CAC အင္တ F S TCC

ဗ္ဗဗ္ဗ r CTG r CTC DGAC V GTG $_{
m L}$ E K AAG I ATC CIC A GCC L CTC CAA R ۳ ک FTT DGAC E 3AG L S AGC A GCC L CTG V GTC D GAC D GAC A GCG GAG Y TAC ဗ္ဗဗ္ဗ P CCG V GTC E CIC R CGC A GCG L CTG AAA DGAC A GCC T CTC R I CGC ATC V GTC E Y TAC ဗ္ဗဋ္ဌ E GAG K AAG A E GCG GAA A K AAG K AAG A GCC Y G GGG GAG ы P H CTC V GTC H ATC н CGC GAC S TCC L CTC CAG Y L D

W CAG DGAC CCC R AGG r CTG ဗ္ဗင္ဗ Y TAC K AAG E GAA W CTT W TGG A GCC P CCG T I ATC L CTC

K AAG V GTC ი წწმ မှ ည CTT N AAC DGAC S TCC E GAG DGAC ი მვმ TACC L CTG A GCC CGG Y TAC GAC 3 3 3 3 4

E CIG s AGC ი ნმ W E GAG E CIG r CTT K AAG R AGG A GCG TACG K AAG EGAG ი ცვვ I ဗ္ဗဋ္ဌ

CTG IATC K AAG E GAG K CGG IATC A GCC ည် K AAG L CTG r CGG D GAC $_{
m L}$ N AAC K AAG CIC r CT A GCC

GAC ACC. က္က V GTG X AAG A GCC r CTG DGAC W TGG န Icc L K AAG LCTG D GAT D GAC M ATG CAC A 3CC

Ы × Д 团 Ы CTT

L ဗ္ဗဋ္ဌ E H CTC LCTC S AGC တ္မင္သ TTT GAG 闰 CTT R AGG GAG L F A 3CC R AGG A . GGG E P P CCC W CCC A GCC E E GAG L CTG A GCC K AAG P S AGC E GAA r CTG

A 3CC L L DGAT A GCC W TGG M ATG မှ သည E K AAG CGC S ICC LCTT V GTG FTT ဗ္ဗဋ္ဌ V GTG F

3 GCC K AAA Y TAT CCT E GAG မှ ငြင်င A GCC r GGG CAC V GTC R ဗ္ဗဗ္ဗ ი მვი R AGG ₽ GCC A GCC A GCC L

L V GTT S AGC r CTG DGAC X AAA A GCC r CTC CIT ი მვმ ය විව GCG E K AAG L CTG DGAC R AGG r CTC

A CTC CTC M ATG P CCC DGAC D GAC ဗ္ဗဗ္ဗ CCC P CCG L g GG G CTT g ggc E GAA R AGG r CHG A GCC 990 Y rg Cg Cg R GGG A GCC V GTG ი მვვ E CCC T T N AAC s TCC PCCT DGAC r CTG r CTC Y TAC

F r GG R AGG E S L CTT A GCC A GCC ස ප E GAG ဗ ဗ္ဗ A 3CG E E ACG W EGAG g 3gg

8 GG GG Y IAC L ₩ TGG L r CTC R AGG E E GAG ი მვმ E r CHT R AGG ი მვვ ¥ M r G N AAC A 3CC

V GTG g 33G TACG A GCC E M ATG CAC A GCC L CTG V GTC A GCT S TCC L P CCC r Agg E V GTG E

IATC E E A GCC V GTG E $_{
m L}$ S TCC L TTG A GCC R AGG CIC Y TAT A GCC V GTG DGAC L CTG RGC

N AAC CTC AAC AAC F P CAC _ရ ရှင်င A GCC L CTG ဗ္ဗင္ဗ $^{
m F}$ V GTC e Gag A GCC E L မှ ငြင် 3CC

A GCC CIT r CTA E FTTT LCTC V GTC GAA r CTG CAG R GG အ ည်

₽ CC L E ۳ ا Y CAG $_{\rm L}$ I ATC K AAG E V GTG I ATC ည် H A 235 E အင္တ r Gr

T ACG R AGG P CCC CAC IATC CIC D GAC CCG L TTG မှ ည D I ATT Y TAC T ACC S AGC K AAG L K AAG

SAGT CIA R AGG ი ცვე T ACG A GCC T ACG A GCC TACG CAG N AAC F R T ACC CAC LCTC အ ပင္ပ ဗ္ဗင္ဗ

S AGC

R AGG Y TAT O CAG DGAC r CTG g GGG A GCC L V GTG P T ACC L TTG L GGC GGC V GTC ₩ TGG CCC ი მვვ IATC E GAG N AAC GAG Q CAG A GCC L CTC IATC N AAC F က် A GCC D GAT R CGG S TCC GGC GGC I ATC

IATC L N AAC GAG DGAC g GGC S TCC CTC CAC A GCC CIG V GTG R AGG L E I ATA O CAG

S AGC

F IATC M ATG ACC. W K AAG s AGC A GCC A GCC A GCG T ACC ය ලේල E င္ပင္ပင TACG M ATG CAC L I ATC မှ လ D GAC D CGG V GTG A GCC ව විරිලි E E GAG CAG cgg F က် က V V GTC R GGG ဗ္ဗဗ္ဗ A LCTA E o CAG s TCC CTC ස විට CAC A GCC S TCG M ATG ඉදිර Y r CTC V GTC G GGG F N AAC

P F SAGC CAG F TTT Y TAC GGC E I ATT F A GCC Q CAG A GCC E EGAG Y PCCT I ATC

Y ი წმ R CGG AGG R AGG စ ဗိ E E L CTG T ACC K AAG E I ATT W A GCC ۳ کا کارک V GTG AAG AAG

V 3TG r GGG A 3CC E LCTA GAC P CCA V GTG Y အင္အင္အ R မှ ဥ ი მვი F I CHC T ACC E GAG V GTG

CAG V GTC P CCC M ATG N AAC FTC A GCC M ATG GGC R E A GCC gcg E GAG R CGG V GTG s AGC K AAG 18 54 36 108 54 162

V K V E D I K L A I K S GIT AAG GTC GAA ATT AAG AGC

K T AAG ACC

Figure 17D

Pfu DNA Polymerase (WT) -(HMf-like) fusion protein [Fig.17-D]

Nucleotide sequence (SEQ ID NO: 61) //Nucleotide sequence (SEQ ID NO: 63)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tenteeenga

aagattgaga tgttcttgg //

54 108 162 GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GTT AAG GTC GCA ATT AAG CTC GCA ATT AAG AGC TGA AAA GCT A //ATG ATG

Figure 17E

(HMf-like) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-E]

Nucleotide sequence (SEQ ID NO: 63) //Nucleotide sequence (SEQ ID NO: 61)

54	108	162	
GGT	GAA	AGA	
GCT	GAG	GGT	
AAG	CTT	GCA	
AGA	CAC	CAC	<u> </u>
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA	CTT	CTT	ATT
GAC	GTA	GAT	GCA
GTT	AAG	GTA	CTC
CCA	GCI	GCA	AAG
၁၁၁	GCA	AAG	ATT
ATT	CAA	AAA	GAC
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GTC
GAA	GTT	GAG	AAG
GGA	AGA	ATT	GTT
ATG	CAG	GCT	ACC
ATG	GCT	AAA	AAG

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga ttacataact gaagaaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt

ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tentecenga acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagagta gatgctacct ttccgggaagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa TGA aagattgaga tgttcttgg //

Figure 17F

(HMf-like) - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-F]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 27) //Nucleotide sequence (SEQ ID NO: 28) Nucleotide sequence (SEO ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	
ggT	GAA	AGA	
GCT	GAG	GGT	
AAG	CTT	GCA	
AGA	CAC	CAC	=
ATA	GAG	AAG	AGC
CTT	GCA	GCA	AAG
AGA	CTT	CIT	ATT
GAC	GTA	GAT	GCA
GTT	AAG	GTA	CIC
CCA	GCT	GCA	AAG
ggg	GCA	AAG	ATT
ATT	CAA	AAA	GAC
CCA	GAG	GCA	GAA
TTA	AGC	ATC	GTC
GAA	GTT	GAG	AAG
GGA			GTT
ATG			ACC
ATG		AAA	AAG

//ATGATITIAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240

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1380
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                                                                                                                                                 GGCAACTTAT
                                                                                                                                                             TGGACAACCT
                                                                                                                                                                                         TCAAAGAAGG
                                                                                                                                                                                                                     CAATGTTTCT
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                                                                                                                                                                                                                                                                                       GGGAAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTCTTCCA
                           TCTTGCCTTC
                                        TATAATGATT
                                                                                ATATTTAGCG
                                                                                             CGAGCCCAAG
                                                                                                          TTTCGACTTG
                                                                                                                                     AGCCTGGGAA
                                                                                                                                                                           ACTTAGGAAA
                                                                                                                                                                                                       GTGGGAAAAC
                                                                                                                                                                                                                                  AGTAGGCCAC
                                                                                                                                                                                                                                              GTTAGAGGAA
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AGAAAAAGTT
              AAAGAGATAC
                                                     TCTTCCATAC
                                                                   TATCAGGGAG
                                                                                                                        TGTATATGAA
                                                                                                                                                                                                                                                                                                    CCTCTACATT
CCACTATTAG
                                                                                                                                                                                                                                                                                                                                                                                                              TAAAGCCAGG
             TTCCATTTGC
                          GGGGAAGAAG AGCTAAAGAT
                                        AAGGCCCAAT
                                                    AAAACATAGA
                                                                 TTCTCAGGAT
                                                                               TCGCATTCCC
                                                                                                         GAAGAATACA
                                                                                                                                     AGATAGCAAA
                                                                                                                                                                           AGTGGTTCTT
                                                                                                                                                                                                      AAAAGGGGTT
                                                                                                                                                                                                                                  TCGCTCCTCA
                                                                                                                                                                                                                                                                        TCTACGGATA
                                                                                                                                                                                                                                                                                                                 GTGAGGAAAT
                                                                                                                                                                                                                                                                                                                                            GGTATGCAGT
                                                                                                                                                                                                                                                                                                                                                                                   ATGAAATTCC
                                                                                                                                                                                                                                                                                                                                                                                                 ATAAGGCGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACAGAAAGG AAGACCTCAG
                                                                                             GAGATGGAAG
                                                                                                                      CACTAGAGGC
                                                                                                                                                 AAGATGCAAA
                                                                                                                                                                                                                     TAATTACCCA
                                                                                                                                                                                                                                              TGGGACATTT
                                                                                                                                                                                                                                                           CTATAGAAAA
                                                                                                                                                                                                                                                                                       TTACTGCCTG
                                                                                                                                                                                                                                                                                                                                                         GAGATTGGAG
                                                                                                                                                                                                                                                                                                                                                                     ACGGAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGAACCA
                                                                                                                                                              CAAGATTAGT
                                                                                                                                                                                         AAGAGGAGTA
                                                                                                                                                                                                                                                                                                    GATTTAAAGT
                                                                                                                                                                                                                                                                                                                               GACTGCTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                            GGCCAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
CAAGATXXXC
                                         GAGTTTGGAA
                                                                                                                                   TACGCCGACG
                                                                                                                                                                                                      AAAGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                TTACATGAGT
                                                                                                                                                                                                                                                                                                                                                                                                              GGAGTTAAAA
                                                                               GGAGACTCAT
                                                                                             ACCATTGGAA
                                                                                                                                                 TACTCGATGG
                                                                                                                                                                           AACCTTGTAG
                                                                                                                                                                                         AAGCCAAGTG
                                                     ATTACTTGGA
                                                                                                                                                                                                                                  AACTATGATA
                                                                                                                                                                                                                                                                                       GCTGAGAGCG
                                                                                                                                                                                                                                                                                                                                                                                   CTTGCCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                            ATTAGCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATATTACA
              GAATACGATA
                                                                   ATAAAGAGAT
                                                                                                         GAAGTCAAGG
                                                                                                                                                             ATTCAGCTTT
                                                                                                                                                                                                                     CCCTCGATTA
                                                                                                                                                                                                                                              CCAAGTCTCT
                                                                                                                                                                                                                                                           ACTCAAGATC
                                                                                                                                                                                                                                                                         GCAAATTCTT
                                                                                                                                                                                                                                                                                                    GAAAAGTTTG
                                                                                                                                                                                                                                                                                                                 GGAGGAGAAA
                                                                                                                                                                                                                                                                                                                               AAGCTCCCTG
                                                                                                                                                                                                                                                                                                                                           ACGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                         ATAGTTAGGA
                                                                                                                        CCAACATACA
                                                                                                                                                                                                                                                                                                                                                                      ATACTAAAAC
                                                                                             GATTAAATTA
                                                                                                                                                              TCCAATGGAA
                                                                                                                                                                                                      TGGATTCGTT
                                                                                                                                                                                                                                GGGATGCAAG
                                                                                                                                                                                                                                                                                                                                           ATTCTTCGTT
                                                                                                                                                                                                                                                                                                                                                         TGGTTTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                            CGATGGTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGATTTGGA
GGAACATCCC
                           ACCAATGGAG
                                        CGAAGGAGAA
                                                    AGCAAAGGTG
                                                                 GAGAGAGATG
                                                                                TACTTATAAT
                                                                                                         GACGGCTGTA
                                                                                                                                     GGAGAAGGTA
                                                                                                                                                 AGTTGCCAAA
                                                                                                                                                                           AAGCACAGGG
                                                                                                                                                                                         AGCTCCAAAC
                                                                                                                                                                                                                                              TGGTTTTATA
                                                                                                                                                                                                                                                             AATGAAGGAA
                                                                                                                                                                                                                                                                          AAAACTCTTA
                                                                                                                                                                                                                                                                                      TAAGGAGTGT
                                                                                                                                                                                                                                                                                                                                                                    TTTGGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                 AACAAGACCA
                                                                                                                                                                                                                                                                                                                                                                                                              AGCTGCTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                        GTATGACGCA
                                                                                                                                                                                                                     AGCCCTATAT
                                                                                                                                                                                                                                                                                                                 AACTATCCCA
                                                                                                                                                                                                                                                                                                                               CATAAATTCA
              GGACATCTTC
                                                                                                                        AATAAATCTC
                                                                                                                                                                                                                                                                                                    GGAGCTCGAA
                                                                                                                                                                                                                                                                                                                                                                                    AATACAAAAG
                                                                                                                                                                                                                    TAGATTTTAG
                                                                                                                                                                                                                                                                        AAAAAGCGAT
AACTTTATT
                                                                                                                                                                           TTTCAAGGTC
                                                                                                                                                                                                      GCTACACAGG
                                                                                                                                                                                                                                                                                                                                           ATAAGAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                              CAAAGAAACT
                           AAGGCCTAAT
                                        CCCTCTATCA
                                                                                                                                                 ACCTTGAGAG
                                                                                                                                                                                         GAAACGAAGT
                                                                                                                                                                                                                                              AGGACATCCC
                                                                                                                                                                                                                                                                                                                 GTCTCTATGC
                                                                                                                                                                                                                                                                                                                                                                                    TAAAAGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                 ATGAGCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                             TACTTAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGATATTGGA
              CAGCAGTTGT
                                                     ATGAAAATGA
                                                                 TATCAAGCGA
                                                                               ACATTATAGT
                                                                                            AAAAACTTGG
                                                                                                          TAGGCGATAT
                                                                                                                        TAACAAGGAC
                                                                                                                                   GAAAGCCAAA
                                                                                                                                                              AAGAATTCCT
                                                                                                                                                                                                                                  TAAATCTTGA
                                                                                                                                                                                                                                                             TTAAGACAAA
                                                                                                                                                                                                                                                                                       GATGGTACTG
                                                                                                                                                                                                                                                                                                    TAGTATGGAA
                                                                                                                                                                                                                                                                                                                               TTGTAAAATA
                                                                                                                                                                                                                                                                                                                                                         TCATTACTCG
                                                                                                                                                                                                                                                                                                                                                                      AAGCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAAGACAAG
ACCGTGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGATCCCA
                                                                                                                                                                                                                                              AAGTTCTGCA
                                                                                                                                                                                                                                                                        GACTATAGAC
                                                                                                                                                                                                                                                                                                                             GCTCTAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                CTCGCAATAT
                          CTCATCGACA
                                        GATATAGAAA
                                                                 GTTGAGGTTG
                                                                               AAGGATCCTG
                                                                                             AAAAGGGCAG
                                                                                                                                    GCAATTTTTG
                                                                                                                                                  AGTGGAGAGA
                                                                                                                                                              GAACTCGGGA
                                                                                                                                                                                                      CTCAGGGAGA
                                                                                                                                                                                                                    ATAGTATACC
                                                                                                                                                                                                                                                             AGACAAAAGA
                                                                                                                                                                                                                                                                                      GCAAAAGCAA
                                                                                                                                                                                                                                                                                                                 GACACTGATG
                                                                                                                                                                                                                                                                                                                                            GAAGGGTTTT
                                                                                                                                                                                                                                                                                                                                                         GAAGGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                   GTGAGAATAG
                                                                                                                                                                                                                                                                                                                                                                                                              GTAGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                            GGATACATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGTACTTA
              AGAGAACATC
                                                     AGTTATGCAG
                                                                                                          ATGCAGAGAA
                                                                                                                        TATCATGTAA
                                                                                                                                                                            TTATGGGATG
                                                                                                                                                                                         GCCTACGAAA
                                                                                                                                                                                                                                  CCCGATACTC
                                                                                                                                                                                                                                                                                                    TACATCGAGT
                                                                                                                                                                                                                                                                                                                                                                      AAAGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // TGA
```

Figure 17G

PFU DNA POLYMERASE (V93 R OR E)-(HMf-like) fusion protein [Fig.17-G]

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1320 1500 1020 1200 1260 1380 1440 1560 1620 1080 1140 1680 1800 780 840 900 960 AAAGAAAAAG AAGGCATGGA TCTTGCCTTC TATAATGATT TGTATATGAA TCAAAGAAGG AGTAGGCCAC GGGAAGAAAG CCTCTACATT GCTTGAATAT TGAAATTGCA TGAAGAAGCT CTGTTATTAG GCTATTCAAA CATTTACGCT TCTTCCATAC ATATTTAGCG CGAGCCCAAG TTTCGACTTG AGCCTGGGAA GGCAACTTAT TGGACAACCT ACTTAGGAAA CAATGTTTCT GTTAGAGGAA AATAGATGAA ACCAGAGAAG CAAGCCTATT AGAAAAGTT AAAGAGATAC TATCAGGGAG AATACTCCTT TTATGGCTAT GTGGGAAAAC GLUTAMIC ACID) TAACGGGGGA CTTGCCAATT ATGAAATTCC AAGGCCCAAT AGTGGTTCTT AAGCCAAGTG AAGAGGAGTA ACGGAGATGT TTAGACCATA AGTTTCTCGG CCACTATTAG TTCCATTTGC AGCTAAAGAT AAAACATAGA TTCTCAGGAT TCGCATTCCC GAGATGGAAG GAAGAATACA CACTAGAGGC AGATAGCAAA AAGATGCAAA CAAGATTAGT TAATTACCCA TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA TTACTGCCTG GTGAGGAAAT GACTGCTAGA GGTATGCAGT GAGATTGGAG AAAAGGGGTT GATTTAAAGT GTTAAGAAAA GGGGAAGAAG GAGTTTGGAA ATTACTTGGA GGAGACTCAT TACTCGATGG AACCTTGTAG AAAGAGCCAG CCCTCGATTA GCTGAGAGCG ATACTAAAAC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GTTGAGAAAA ATAAAGAGAT CCAACATACA TACGCCGACG ATTCAGCTTT CCAAGTCTCT GAAAAGTTTG GGAGGAGAAA GAAGGAAAAC GATAGAACTT CAAGATXXXC GAATACGATA GAAGTCAAGG AACTATGATA ACTCAAGATC AAGCTCCCTG TGGTTTAGAG ATAGTTAGGA ACCATTGGAA GCAAATTCTT cec, cee, ACGAAGAAGA V93R MUTANT: XXX = AGA, AGG, CGA, ATGATITIAG ATGTGGATIA CATAACTGAA AAGCACAGGG AGCTCCAAAC GGGATGCAAG AATGAAGGAA CATAAATTCA AAGCTAGAGT TTTGGAGACA TAAAAGAAGT AATACAAAAG ATGATTCAAA GATTGAAGAA TGTAGAGAAG GGACATCTTC ACCAATGGAG AGCAAAGGTG TACTTATAAT GATTAAATTA GACGGCTGTA TCCAATGGAA AGCCCTATAT AACTATCCCA GAAAATTTAA GATAGAGCAT GGAACATCCC CGAAGGAGAA GAGAGAGATG AATAAATCTC GGAGAAGGTA AGTTGCCAAA TGGATTCGTT TGGTTTTATA AAAACTCTTA TAAGGAGTGT ATTCTTCGTT GGAGCTCGAA TTAAGACAAA GAATTGTTGA ATGAAAATGA TAACAAGGAC ACCTTGAGAG TTTCAAGGTC GAAACGAAGT TAGATTTTAG AGGACATCCC AAAAGCGAT GATGGTACTG GTCTCTATGC TCATTACTCG CAGCAGTTGT AAGGCCTAAT ACATTATAGT AAAAACTTGG TAGGCGATAT AAGAATTCCT GCTACACAGG TAGTATGGAA ATAAGAGGGG AACTTTATTT CCCTCTATCA GAAAGCCAAA TAAATCTTGA TTGTAAAATA TATCAAGCGA CTTCTCAGGG AAAGAGAACG AAAGAAACTC GTGAGAATAG CCCGATACTC AAGTTCTGCA AGACAAAAGA GAAGGAAAAG AAGATTGTGA ACCGTGTGGA AGTTATGCAG AAAAGGGCAG TATCATGTAA TTATGGGATG CTCAGGGAGA ATAGTATACC GACTATAGAC AGAGAACATC GATATAGAAA AAGGATCCTG ATGCAGAGAA AGTGGAGAGA GAACTCGGGA GCCTACGAAA TACATCGAGT GACACTGATG GCTCTAGAAT GAAGGGTTTT CTCATCGACA GTTGAGGTTG GCAATTTTG GCAAAAGCAA

108 162 //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 2100 2328 CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GTAGCTGTTG

Figure 17H

PFU DNA POLYMERASE (G387P/V93R OR E) - (HMf-like) fusion protein [Fig.17-H]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 540 9 GGCAACTTAT 960 G387P Mutant (CCN is the codon for Proline where $N=C,\ G,\ A,\ or\ T)$ ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CCACTATTAG AGAAAAGTT CAGCAGTIGI GGACAICTIC GAATACGATA ITCCATTIGC AAAGAGATAC CATTTACGCT AAGGCATGGA CAAGCCTATT TCTTGCCTTC TCTTCCATAC TATCAGGGAG ATATTAGCG TTTCGACTTG TGTATATGAA AGCCTGGGAA TGGACAACCT TATAATGATT CGAGCCCAAG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TTAGACCATA GGAGACTCAT TCGCATTCCC TAACGGGGGA GAATIGITGA TGTAGAGAAG GITGAGAAAA AGITICICGG CACTAGAGGC SAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT AAAACATAGA TTCTCAGGAT AGATAGCAAA AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GAGATGGAAG GAAGAATACA AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT GTTAAGAAAA AACTITATIT GGAACAICCC CAAGAIXXXC GAGTTTGGAA AGCAAAGGTG ATTACTTGGA GAGAGATG ATAAAGAGAT GATTAAATTA ACCATTGGAA GAAGTCAAGG TACGCCGACG CCAACATACA ATGATTCAAA GATTGAAGAA CGAAGGAGAA AAGGCCTAAT ACCAATGGAG GACGGCTGTA TAACAAGGAC AATAAATCTC GGAGAAGGTA TACTTATAAT ATGAAAATGA ACATTATAGT AAAAACTTGG TAGGCGATAT CCCTCTATCA GAAAGCCAAA TATCAAGCGA CTTCTCAGGG AAGATTGTGA ACCGTGTGGA AGAGAACATC CTCATCGACA GATATAGAAA AGTTATGCAG AAGGATCCTG AAAAGGGCAG TATCATGTAA GCAATTTTG GTTGAGGTTG ATGCAGAGAA

1620 1680 2100 1860 2160 2280 1200 1260 1440 1500 1560 1380 1740 1800 1920 1980 2040 2220 ACTTAGGAAA TCAAAGAAGG GTGGGAAAAC CAATGTTTCT AGTAGGCCAC GTTAGAGGAA AATACTCCTT GGGAAGAAAG CCTCTACATT AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA TGAAGAAGCT ACCAGAGAAG AGGTCCTCAC AGCTGAGGAA GGTTCTTCCA TACAGAAAGG AAGACCTCAG ATACCAAAAG TTATGGCTAT AATGGTAATT TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII CTTGCCAATT ATGAAATTCC NGGATICGIT AAAGAGCCAG AAAAGGGGTT TCTACGGATA GATTTAAAGT GTGAGGAAAT GGTATGCAGT ATAAGGCGAT TAAAGCCAGG GGGCAATTCT AAGAGGAGTA TAATTACCCA TCGCTCCTCA TGGGACATTT CTATAGAAAA TTACTGCCTG GACTGCTAGA GAGATTGGAG ACGGAGATGT TGGAGAACCA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // TTACATGAGT AAGCCAAGTG ACGAAGAAGA ATAGTTAGGA ATACTAAAAC CCCTCGATTA CCAAGTCTCT ACTCAAGATC GCTGAGAGCG GAAAAGTTTG AAGCTCCCTG GGAGTTAAAA ATTAGCAATA GAATATTACA AACTATGATA GCAAATTCTT GGAGGAGAAA TTTGGAGACA GGGATTTGGA AGCTCCAAAC AGCCCTATAT GGGATGCAAG CATAAATTCA ATTCTTCGTT TGGTTTAGAG AACAAGACCA AGCTGCTAAA CGATGGTCCA GTATGACGCA TGGTTTTATA AATGAAGGAA AAAACTCTTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA AATACAAAAG TAAAAGAAGT AAAAAGCGAT GATGGTACTG GTCTCTATGC TCATTACTCG AAGCTAGAGT ATGAGCAGAT CAAAGAAACT TACTTAGAGG GAAACGAAGT GCTACACACC TAGATTTTAG TAAATCTTGA AGGACATCCC TTAAGACAAA TAGTATGGAA TTGTAAAATA ATAAGAGGGG GGATATTGGA AAAAGCACAA GACTATAGAC GCGGTACTTA ACAAGACAAG TTATGGGATG CTCGCAATAT **TACGATCCCA** CTCAGGGAGA ATAGTATACC GACACTGATG GCTCTAGAAT GAAGGGTTTT AAAGAAACTC GTGAGAATAG GTAGCTGTTG GGATACATAG GCCTACGAAA CCCGATACTC AAGTTCTGCA AGACAAAAGA **FACATCGAGT** GAAGGAAAAG GCAAAAGCAA

108 //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG ACC GIT AAG GIC GAA GAC AIT AAG CIC GCA AIT AAG AGC IGA

Figure 17

(HIMf-like) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein ${
m [Fig.17-I]}$

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 29) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 30)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) G387P Mutant (CCN is the codon for Prolline where $N=C,\ G,\ A,\ or\ T)$

108 162

> 1080 1200 1380 1020 1140 1260 1320 1560 1620 1680 1860 2100 1440 1500 1740 1800 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 540 900 840 900 960 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAAGAAAAG CAAGCCTATT AACTITATIT GGAACATCCC CAAGATXXXC CCACTATIAG AGAAAAGTT AAAGAGATAC ATATTTAGCG AGCCTGGGAA GGCAACTTAT TGGACAACCT TCAAAGAAGG GTGGGAAAAC CAATGTTTCT AATACTCCTT TTATGGCTAT GGGAAGAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA TGAAGAAGCT ACCAGAGAAG AGGTCCTCAC GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT TCTTGCCTTC TATAATGATT TATCAGGGAG CGAGCCCAAG TTTCGACTTG TGTATATGAA ACTTAGGAAA AGTAGGCCAC GTTAGAGGAA CCTCTACATT TCTTCCATAC CAGCAGTIGI GGACAICTIC GAATACGATA IICCAITIGC AGATAGCAAA ATGAAATTCC ATAAGGCGAT AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TTCTCAGGAT TACTTATAAT GGAGACTCAT TCGCATTCCC GAAGAATACA AGTGGTTCTT GGGATGCAAG AACTATGATA TCGCTCCTCA TCTACGGATA GTGAGGAAAT GGTATGCAGT GAGATTGGAG TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT GATTAAATTA ACCATTGGAA GAGATGGAAG CACTAGAGGC CAAGATTAGT NGGATTCGTT AAAGAGCCAG AAAAGGGGTT TAATTACCCA CTATAGAAAA TTACTGCCTG GATTTAAAGT ATTACTTGGA AAAACATAGA AAGATGCAAA AAGAGGAGTA TGGGACATTT GACTGCTAGA ACGGAGATGT AGCTCCAAAC AAGCCAAGTG GAGAGATG ATAAAGAGAT GAAGTCAAGG CCAACATACA TACGCCGACG AGTTGCCAAA TACTCGATGG TCCAATGGAA ATTCAGCTTT AAGCACAGGG AACCTTGTAG CCCTCGATTA CCAAGTCTCT ACTCAAGATC AAAACTCTTA GCAAATTCTT GCTGAGAGCG GAAAAGTTTG GGAGGAGAAA AAGCTCCCTG ATTCTTCGTT ACGAAGAGA TGGTTTAGAG ATAGTTAGGA ATACTAAAAC CTTGCCAATT CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT AGCAAAGGTG AGCCCTATAT TTTGGAGACA GACGGCTGTA GGAGAAGGTA TGGTTTTATA AATGAAGGAA CATAAATTCA TAAAAGAAGT AATACAAAAG AATAAATCTC TAAGGAGTGT GGAGCTCGAA AACTATCCCA GAATTGTTGA CCCTCTATCA ATGAAAATGA ACATTATAGT AAAAACTTGG TAACAAGGAC GAAAGCCAAA ACCTTGAGAG AAGAATTCCT TTTCAAGGTC GCTACACACC TAGATTTTAG TAAATCTTGA TTAAGACAAA AAAAAGCGAT TAGTATGGAA TATCAAGCGA GAAACGAAGT AGGACATCCC GATGGTACTG GTCTCTATGC ATAAGAGGGG TCATTACTCG AAGCTAGAGT TAGGCGATAT TTGTAAAATA CTCATCGACA AAAAGGGCAG GACTATAGAC GATATAGAAA AAGGATCCTG GAACTCGGGA TTATGGGATG CTCAGGGAGA ATAGTATACC AAGTTCTGCA AGACAAAAGA GAAGGGTTTT GAAGGAAAAG AAAGAAACTC GTGAGAATAG AAGATTGTGA ACCGTGTGGA AGAGAACATC AGTTATGCAG GTTGAGGTTG ATGCAGAGAA GCAATTTTTG AGTGGAGAGA CCCGATACTC GACACTGATG GCTCTAGAAT TATCATGTAA GCCTACGAAA GCAAAAGCAA TACATCGAGT

GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GGATATIGGA GGGATITGGA TACAGAAAGG AAGACCICAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG AAAAGCACAA TACGATCCCA GCGGTACTTA

Figure 17J

(HMF-LIKE) - PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein Fig.17-J

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG ACC GIT AAG GIC GAA GAC AIT AAG CIC GCA AIT AAG AGC //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 240 480 540 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 CTICTCAGGG ATGATICAAA GATIGAAGAA GTIAAGAAAA TAACGGGGGA AAGGCAIGGA 180 900 TATAATGATT IATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA CAAGCCTATT AGAAAAGTT TCTTGCCTTC TCTTCCATAC ATATTTAGCG CGAGCCCAAG TTTCGACTTG AAAGAGATAC TATCAGGGAG TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG TTCCATTTGC CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT AGCAAAGGTG ATTACTTGGA AAAACATAGA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TCGCATTCCC ACCATTGGAA GAGATGGAAG CAAGATXXXC GAATACGATA GGAGACTCAT GGACATCTTC GATTAAATTA GGAACATCCC TACTTATAAT CAGCAGTTGT GAATTGTTGA ACCGTGTGGA AACTTTATTT AAGGCCTAAT CCCTCTATCA ATGAAAATGA AAAAACTTGG TATCAAGCGA ACATTATAGT AGTTATGCAG AAGGATCCTG AAAAGGGCAG GCNATAGCNA AAGATTGTGA AGAGAACATC CTCATCGACA GTTGAGGTTG ATGCAGAGAA

GCTACACA [CCN] GGT_GGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII ACIIAGGAAA 1080 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATITITAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTITCT 1260 1440 1560 1680 1740 1800 1860 1920 1980 2040 2100 2160 AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020 1320 1500 1620 TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC GTTAGAGGAA GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA AATACTCCTT TTATGGCTAT TGAAGAAGCT ACCAGAGAAG AGCTGAGGAA GGCAACTTAT GGGAAGAAAG CCTCTACATT AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA AGGTCCTCAC AATGGTAATT GGTTCTTCCA ATACCAAAAG TCTACGGATA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGTATGCAGT GAGATTGGAG TITGGAGACA ATACTAAAAC ACGGAGATGT ATGAAATTCC TGGAGAACCA TACAGAAAGG AAGACCTCAG AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT CTATAGAAAA GAAAAGTTTG GATTTAAAGT GTGAGGAAAT GACTGCTAGA ATAAGGCGAT TAAAGCCAGG GGGCAATTCT GCTGAGAGCG TTACTGCCTG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // ACTCAAGATC GCAAATTCTT GGAGGAGAAA ACGAAGAAGA ATAGTTAGGA CTTGCCAATT TTACATGAGT GGAGTTAAAA GTATGACGCA GAATATTACA AAGCTCCCTG CGATGGTCCA ATTAGCAATA GGGATTTGGA AATGAAGGAA ATTCTTCGTT TAAGGAGTGT AACTATCCCA CATAAATTCA TGGTTTAGAG AACAAGACCA AAAACTCTTA GGAGCTCGAA AATACAAAAG AGCTGCTAAA AAAAAGCGAT ATAAGAGGG AAAAGCACAA GGATATTGGA TTAAGACAAA GATGGTACTG TAGTATGGAA GTCTCTATGC TTGTAAAATA TCATTACTCG AAGCTAGAGT TAAAAGAAGT ATGAGCAGAT CAAAGAAACT TACTTAGAGG ACAAGACAAG GACACTGATG TACGATCCCA AGTGGAGAGA GAACTCGGGA GCAAAAGCAA TACATCGAGT GCTCTAGAAT GAAGGAAAAG GTGAGAATAG CTCGCAATAT GGATACATAG GCGGTACTTA TTATGGGATG GCCTACGAAA CTCAGGGAGA ATAGTATACC CCCGATACTC AAGTTCTGCA AGACAAAAGA GACTATAGAC GAAGGGTTTT AAAGAAACTC GTAGCTGTTG

TGA

Figure 17K

(HMF-LIKE) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E) Fig.17-K]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GCTACACA [CC N] GGTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 1080 1320 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 1620 1680 1800 1860 2160 TGGACAACCT 1020 1440 1500 1560 1740 2040 900 9 720 840 900 GGCAACTTAT 960 ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CGAGCCCAAG AGCCTGGGAA ACTTAGGAAA TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC AATACTCCTT CATTTACGCT TCTTGCCTTC TATCAGGGAG TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG TTTCGACTTG TGTATATGAA GTTAGAGGAA TTATGGCTAT GGGAAGAAAG AAAGAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA ACCAGAGAAG AGGICCICAC AATGGTAATT TACTIAGAGG CGAIGGICCA AITAGCAATA GGGCAATICI AGCIGAGGAA CAAGCCTATT AGAAAAGTT AAAGAGATAC TATAATGATT TCTTCCATAC CCTCTACATT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA TGAAGAAGCT TITCAAGGIC AAGCACAGGG AACCIIGIAG AGIGGIICII CTATAGAAAA GGACATCTTC GAATACGATA TTCCATTTGC TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TACGCCGACG AGATAGCAAA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG TTAGACCATA CCACTATTAG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TTCTCAGGAT GAGATGGAAG CACTAGAGGC ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA TCTACGGATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GGTATGCAGT TGGTTTAGAG ATAGTTAGGA GAGATTGGAG ATGAAATTCC AGTTTCTCGG CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT GCTGAGAGCG TTACTGCCTG GTGAGGAAAT TITGGAGACA ATACTAAAAC ACGGAGATGT TGGGACATTT GATTTAAAGT GAAAATTTAA GATAGAGCAT GATAGAACTT GTTGAGAAAA CAAGATXXXC ATAAAGAGAT AAAAACTTGG GATTAAATTA ACCATTGGAA CCAACATACA CCAAGTCTCT TTAAGACAAA AATGAAGGAA ACTCAAGATC AAAAAGCGAT AAAACTCTTA GCAAATTCTT GAAAAGTTTG GGAGGAGAAA ACGAAGAAGA CTTGCCAATT ATTCTTCGTT TGTAGAGAAG GGAACATCCC GAGAGAGATG TAACAAGGAC AATAAATCTC GGAGAAGGTA AGGACATCCC TGGTTTTATA GATGGTACTG TAAGGAGTGT GGAGCTCGAA AACTATCCCA TAAAAGAAGT AATACAAAAG AACTTTATTT AAGGCCTAAT ACATTATAGT GAAAGCCAAA TAGTATGGAA GTCTCTATGC TTGTAAAATA ATAAGAGGGG CAAAGAAACT GAATTGTTGA CAGCAGTTGT CCCTCTATCA TATCAAGCGA TCATTACTCG AAGCTAGAGT GGATACATAG AAAGAGAACG CTTCTCAGGG AGTTATGCAG AGTGGAGAGA GAACTCGGGA ATAGTATACC CCCGATACTC AGACAAAAGA GACTATAGAC TACATCGAGT GCTCTAGAAT GAAGGGTTTT AAAGAAACTC CTCGCAATAT GTAGCTGTTG AAGATTGTGA AGAGAACATC GCNATAGCNA AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCCTACGAAA CTCAGGGAGA AAGTTCTGCA GCAAAAGCAA GAAGGAAAAG ACCGTGTGGA CTCATCGACA TTATGGGATG GACACTGATG GTGAGAATAG GTTGAGGTTG GCAATTTTTG

2280 2328 IACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GGATATTGGA GCGGTACTTA

108 162 54 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17L

KOD DNA POLYMERASE - (HMf-like) fusion protein [Fig.17-L]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 1140 1200 540 999 840 300 360 900 720 900 CTGTCATAAG AATTTTCAAG GAGGCACGGG CCTTATGATA GGTCACATAC CGGCCAGTCC CCTCAGGAAG GGAGAACATA TIGAACCCIA CITCIACGCC GAGACCAGTT GGACAAGATA CAAGCGCTAC TCTCCCCTAC CTATCTGAAA CGAGCCGAAG CGTTTATGAA AGCCTGGGAA GGCCAGAAGA GCTCGCCTTC CTTCGATCTC TGTGAAGGAG GLUTAMIC ACID) CTATGTAAAA GAGCCCGAGA GAGGGTTGTG TAACCGCCGA CAGCGATAAG AAATAACCAC TACCCTTCGC TCCTCCGTGT CGCTTGAGGC AGTICCICGG GGCGACGAGG AGCTGAAAAT AGGGGCCAAT AGAACGTGGA TCGACTTCGC GGGATGGAAG GACGGATACA AAGATGCGAA CTCGCTTAAT AAAAGGAGCT AGTGGTTCCT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT CATTGAGGAA GTCAAGAAGA GTTCAGAAGA CAGGACXXXC GAGTTCGCCG ATAAAGCGCT GGCGACAACT TACGCTGAGG CAGCACTGGC AACCTCGTTG AAGCCCGATG GAGTACGACA ATAACTTGGA GCCCTCGGAA TACTCGATGG GAAGTGAAGG CCCACATACA TCCGATGGAG GCCCAGCTTT TACTCATCCG TGAGGGCGAG GAGGGAGATG GGAGAAGGTT GGCCCCGAAC GGTTGAAAG TGACATCTAC GGCCAGGGTG AACCTACAAC AATAAACTTC AGTCGCCCGC GCCAATGGAA GTTTGCCGTC GATAAACCTG CGGTTAAGCG AACTCTACTT AAAAGCTCGG CAGCAGTTAT AGGGATTAGT ACGAGGAAGG ACGLICICAL TGGGCGACAG ACCTTGAGAG AGGAGTTCCT TCTCCCGCTC ATGAAGGAGG CTCCTGAAGG ACGATTCTGC CTCTCTACCA TCTCGACGGA TAAGACGGAC GTCAGCCGAA GGAATGAGCT ACGGTTGTAA AAAGACCCGG AAGCGCTGTG GAGCTTGGGA GCCTATGAGA CGGCAGAGCT CTCATAGACA GTTGACGTCG ATTCAGAGGA ACCGGCGAGA CTCTGGGACG GAGGTCTGGA CGAGAGCATC GACATTGAAA AGCTACGCCG TATCCTGTGA GCCGTCTTCG

ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA	AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA	AG GCA GTA (GCA AAA AA	ATT GAG ATC	AAA GCT
GAG	STA CTT GCA	'A GCT AAG	GAG CAA GC	AGA GTT AGG	GCT CAG
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT	AC AGA CTT A	CCA GIT G	CCA ATT GCC	SGA GAA TTA	//ATG ATG (
	CT 2325	CCGAAGGGAA	TTGGCTGAAG	AGACAGGTTG GTTTGAGTGC TTGGCTGAAG CCGAAGGGAA CT 2325	AGACAGGTTG
CCAGAAGACG 2280	GTTGAGAGAA TTCTGAGAGC CTTCGGTTAC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG	CGCAAGGAAG	CTTCGGTTAC	TTCTGAGAGC	GTTGAGAGAA
TCTCCCAGCC 2220	GACCCGACGA AGCACAAGTA CGACGCCGAG TACTACATTG AGAACCAGGT	TACTACATTG	CGACGCCGAG	AGCACAAGTA	GACCCGACGA
CGACGAGTTC 2160	CGATACCGTT	GGCGACAGGG	TGGGAGGATA GGCGACAGGG	TACATCGTGC TCAAGGGCTC	TACATCGTGC
GGTGATAAGC 2100	CGCGAGAGGA GTCAAAATAC GCCCTGGAAC GGTGATAAGC	GTCAAAATAC		GCCGTTGCCA AGAGGTTGGC	GCCGTTGCCA
TCCCCACGTT 2040	GTGATCCACG AGCAGATAAC GAGGGATTTA AAGGACTACA AGGCAACCGG	AAGGACTACA	GAGGGATTTA	AGCAGATAAC	GTGATCCACG
GGAGAAGCTG 1980	AGGIICCGCC GGAGAAGCIG	AGCAAGTACG	CGAAAAGCTG	AGGATAGTCA AAGAAGTTAC	AGGATAGTCA
GAAGGCCGTG 1920	CTAAAGGACG GTGACGTCGA GAAGGCCGTG	CTAAAGGACG	TGAAGCTTTG	GAGACGCAGG CGAGGGTTCT	GAGACGCAGG
GATAGCGAAA 1860	GGCAAGATAA CAACGCGCGG ACTTGAGATT GTGAGGCGTG ACTGGAGCGA GATAGCGAAA	GTGAGGCGTG	ACTTGAGATT	CAACGCGCGG	GGCAAGATAA
AGACGAGGAA 1800	ATGCGGTGAT	AAGAAGAAGT	CTTCGTCACG AAGAAGAAGT	GGCTTCTACA AACGCGGCTT	GGCTTCTACA
CGCTTGAGCT CGAGTACGAG 1740		CTTCCGGGCG	CAACGCCAAA CTTCCGGGCG	ATGGAGTTCC TCAAGTATAT	ATGGAGTTCC
AAAGAAGGCT 1680	ACCGACGGAT TITITGCCAC AATACCTGGA GCCGATGCTG AAACGTCAA AAAGAAGGCT	GCCGATGCTG	AATACCTGGA	TTTTGCCAC	ACCGACGGAT
CTACAGCGAC 1620	TTAAGGTAAT	AAGTACGGCT	GATAGAGGAA AAGTACGGCT	ATAACGATGA CCATCAAGGA	ATAACGATGA
CGGCCTGGGG AAGGGAGTAC 1560		GAGAGCGTAA	GGAGTGTGCA	AGGGCGCGCT GGTACTGCAA GGAGTGTGCA GAGAGCGTAA	AGGGCGCGCT
CGGCTATGCA 1500	ACGGTTACTA CGGCTATGCA	AACAGCTACT	GATCCTGGCA	TACAGGCAGA GGGCCATCAA GATCCTGGCA AACAGCTACT	TACAGGCAGA
TCGAGAGGAA GCTCCTCGAT 1440		ATTGACCCGA	GAAGGCCACG ATTGACCCGA	CAGAAGATAA AGAAGAAGAT	CAGAAGATAA
GAGACCTCCT AGAGGAGAGG 1380		AGCCTGCTTG	ATTTATCCCG	TTCTGCAAGG ACTTCCCAGG ATTTATCCCG AGCCTGCTTG	TTCTGCAAGG
CGGCCACCGC 1320	CCCCACAGGT	TATGACGTTG	ATGCAAGGAA TATGACGTTG	GATACGCTCA ACAGAGAGG	GATACGCTCA
CGICICGCCG 1260	GIGIACCIAG AITITAGAIC CCIGIACCCC ICAAICAICA ICACCCACAA CGICICGCCG	TCAATCATCA	CCTGTACCCC	ATTTAGATC	GTGTACCTAG

Figure 17M

54 108 162

(HMf-like) - KOD DNA POLYMERASE fusion protein [Fig.17-M]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 34)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

```
54
108
162
//ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG GCC GTA AAA AAG GCA GTA AAG CTC GCA ATT AAG AGC //
```

Figure 17N

(HMf-like)-vent DNA POLYMERASE FUSION PROTEIN [Fig.17-N]

Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 36)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC //

1020 1080 1140 1200 1260 1440 840 540 780 AGAGTATAAA AGGTTTGTGG GGACTTAATT CGAAAAGAAA TACTCACAAC TCCGATAGTA CGCATGGGGG AAGGGAAGTT GGGCAAAATA AATAATGATT TTTGCCGTAT AATCCACTTT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GTATCTTTA TATATATGCT GAGACATGGA CAAGCGTTAT TGTTAAAGAA GTATCTCATA GCTGATAGGT AATTTTAAG CCTTGCCTTT ACATCCCGAA GGGTATCCTA AGGCAAGATG GTACTCGAAG GAATGTGCTG AAAGCGTTAC CCGAACAAAC CTGATGAGGA GGCCAGAGTA ATCACATGGA AAAATATCGA ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG TTCAGCCCTA TATTGAGGAG ATAAAGGCAA TAAAGGGCGA TGCAGTGAAA GTCAGGAAAA AATTTTTGGG CGAGCATCCC CAAGACXXXC CAGCTATGCG AGGCCGAGAT TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA AGCTGGCAAA TCGTGGAGTG AGCCAGAAAA CAATAATAGT ACGATGTTGC GAATATGACA TACCCTTTGC GGAGACGAGG AGCTTAAGCT TTGATTTGCC GAAGAAATG AAATCCACAA TTGACCCGAT ACAGCTATTA CCATACTCGG TATGTAAAAG TGTAAGAATT TTGCTTGCAA AACCAAAAGC AAATTAGGAG GGGAGTTTAA AATAGAACTT GACCCTCATT GAATTTGGAA CAGTIGICG AAGGACGAIA AACCICCCAA ATGGAAGCTG ACCGGCAACC CTGTACCCTT ATAAAGCGTT GGGGACAATT GTCTTAGGAA GCTGTGGAAA GAAAAACTA GCCCAGTACT TTTATTCCCT TGAGGGAGAT AAGAGAAATG AGTTCGGCTT TGATAGTTTT GAGATCAAGC AAAAGAGGGC ATTCTTCCCC TGAACTTGCA CCTGGGAGGA CTTTCCGGGC GGCTATTAAA TGACATTTAC TCCCATGGAG TTTCCGCAGT AACTTACAAT ATGACTCCGC GAGTGCTCGA AAAAGCTGGG AGAGGATGGG TTTTAGGAAA TCGGGAAGGA ACGCGAGGAA GCAATGAGGC AAGATATAAA ATAGGCAAAG CAGCTGTGGT TGTCCAATGA ATGTGATAAT AAGAAAGCAT ATACCCTTGA AGGCCTTGAT ATGAAGAAGA GGGACGTCTC GAACAACTTA TTTATTGGA AGCTCATTTT CGTTTTATCA TCTGCAAGGA GTATCCCCAG TATGAAGCAG TGGGAAACAG GAAAATATCA AAAGAGAACG CTCATAGACA AGTTATGCCG AAAGACCCCG CAAAGTGTAT AGGGTGGCAT ATGCTCGATT CTTCTCAAAG AAAACTGTGA GAAGTCTGGA AGGGAACATC GTCGATGTTG AAACGGGCAG CCCAAGATTC GATCTTTTCC ACGTATGAGC CGGCGCTTAA GGATATAGGT GATATTGAAA

2100 2160 1740 1800 1860 1980 2040 1920 2220 ACCGGGCACA TAAGGTTCTT ACTCATTAAA GCTTGAGCTT TGCAGTCATA TTGGAGTGAG AAGTGTTGAA GGTTCCACTT AGCCATTGGC AATTTTACTT AAACCAAGTT TTTAAGGTAT ATAGAGGAAA AGTICGGCTT AGGACTACAA TAAAAGTGAA GAAAGGAGGA AAAAGCCTGA AAACTACATA AACTCCAAAC TTCCAGGTCT TAAGGAGAGA TTAAAGAGGG CAAAATACAG GCGATAGGGT ACTACATAGA AAAAGCGCTA CTTAGATGCA TGGCTCAAGA GGTAG 2325 ATACCCGGGG TTTGTTACAA GAGAAAATAG GCAAGAGGGA TTGGAAGTAG GAGGCTATAC AGGGATTTAA GGAAAGATAA GATCCGGACT TTTGGATACA GATAAGAGAA ACTCGAAGCG TTATGCCACA GAGAGGATTC ACACAAGTAC AACAAGGGGC AAAGGTTTTA AGATGTTGTA GCAGATTACC AAGACTTGCC CAAAGGGAGC AACAAACCGG AGGAATTCCT AAGTTGTTAG TAGAGATGAC CGATAGCAAA TACTTAGGAT CTGACGGCTT GCTTTTACTT GCAGGATAAC AGACTCAGGC TTATCCATGA ATATCGTTCT ATCCTAGAAA **PATGCGGACA** AAGAAAGCCA ACAGAATACG CAAAGCTCAA ATAGCTAAGG AAAGCTGTAG CCTCATGTCG TTGCCGGCAG GAGTATGAGG GATGAAGAGG GAAAAGCTTG ATAATAAGCT

Figure 170

Vent DNA POLYMERASE - (HMf-like) FUSION PROTEIN [Fig.17-O]

// Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO; 63) Nucleotide sequence (SEQ ID NO: 35)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

480 540 009 099 360 TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GAGACATGGA ACATCCCGAA TGAGGCAGTT ATGATACTGG ACACTGATTA CATAACAAA GATGGCAAGC CTATAATCCG AATTTTTAAG TTCAGCCCTA TATATATGCT TTTGCCGTAT TGCTAGGGCA AAGGGAAGTT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT AATAATGATT TGTTAAAGAA GTATCTCATA AATCCACTTT TGCCGCTATA CAATGGAAGA AATTTTGGG TACCCTTTGC AGGGCGAGAT CAGAGGAAAT CAGCTATGCG AAAATATCGA TTGTTCAAGT TTGATTTGCC GGGACAAAGA CGTATACGCT AGCTTAAGCT TCAAGGGTAG GAATTTGGAA GGGAGTTTAA AATAGAACTT GACCCTCATT GTCAGGAAAA GGAGACGAGG GCTGTGGAAA GCCCAGTACT CAAGACXXXC ATCACATGGA GGGGACAATT AAATTAGGAG GAATATGACA ATAAAGCGTT GTCTTAGGAA AACCTCCCAA TGACATTTAC GGCCAGAGTA AACTTACAAT AAGGACGATA GAAAAACTA AAGAGAAATG AACCAAAAGC TGCAGTGAAA CGAGCATCCC TCCCATGGAG AGTTCGGCTT TGAGGGAGAT TGATAGTTTT TGGGAAACAG AAGAAAGCAT ATGACTCCGC CAGTTGTGCG GAGTGCTCGA AGCTCATTTT CAGCTGTGGT AGGCCTTGAT TGTCCAATGA AAAAGCTGGG AGAGGATGGG TTTTAGGAAA CGTTTTATCA ATGAAGAAGA ATGTGATAAT AAAGAGAACG CTTCTCAAAG AAAGACCCCG AAACGGGCAG AGGGAACATC GATATTGAAA AGTTATGCCG CCCAAGATTC GATCTTTCC TATGAAGCAG AAAACTGTGA GAAGTCTGGA CTCATAGACA GTCGATGTTG

		GG 2325 //	TGGCTCAAGA	CTTAGATGCA	CAAAGCTCAA AACAAACCGG	CAAAGCTCAA
2280	TTTAAGGTAT	GAAAGGAGGA	TTTGGATACA	ACTCGAAGCG	TACTTAGGAT	TTGCCGGCAG
2220	AAACCAAGTT	ACTACATAGA	GATCCGGACT	ACACAAGTAC	ATCCTAGAAA	ACAGAATACG
2160	AATTTTACTT	GCGATAGGGT	GGAAAGATAA	CAAAGGGAGC	ATATCGTTCT	ATAATAAGCT
2100	ACCGGGCACA	TAAAAGTGAA	GCAAGAGGGA	AAGACTTGCC	CGATAGCAAA	CCTCATGTCG
2040	AGCCATTGGC	AGGACTACAA	AGGGATTTAA	GCAGATTACC	TTATCCATGA	GAAAAGCTTG
1980	GGTTCCACTT	CAAAATACAG	GAGAAAATAG	AGATGTTGTA	AAGTTGTTAG	AAAGCTGTAG
1920	AAGTGTTGAA	TTAAAGAGGG	GAGGCTATAC	AAAGGTTTTA	AGACTCAGGC	ATAGCTAAGG
1860	TTGGAGTGAG	TAAGGAGAGA	TTGGAAGTAG	AACAAGGGGC	GCAGGATAAC	GATGAAGAGG
1800	TGCAGTCATA	AAAAGCGCTA	TTTGTTACAA	GAGAGGATTC	GCTTTTACTT	GAGTATGAGG
1740	GCTTGAGCTT	TTCCAGGTCT	AACTCCAAAC	AAACTACATA	AGGAATTCCT	AAGAAAGCCA
1680	ACTCATTAAA	AAAAGCCTGA	ATACCCGGGG	TTATGCCACA	CTGACGGCTT	TATGCGGACA
1620	TAAGGTTCTT	AGTTCGGCTT	ATAGAGGAAA	GATAAGAGAA	TAGAGATGAC	AGACACTACA
1560	CGCATGGGGG	AAAGCGTTAC	GAATGTGCTG	GTACTCGAAG	AGGCAAGATG	GGGTATCCTA
1500	CGGCTATATG	ACAGCTATTA	TTGCTTGCAA	GGCTATTAAA	ATAGGCAAAG	ATGCTCGATT
1440	CGAAAAGAAA	TTGACCCGAT	AAATCCACAA	GAAGAAAATG	AAGATATAAA	GCAATGAGGC
1380	GGACTTAATT	CCATACTCGG	TTTATTCCCT	CTTTCCGGGC	TCTGCAAGGA	GGATATAGGT
1320	TCCGATAGTA	ACGATGTTGC	TGTAAGAATT	AAAAGAGGC	ATACCCTTGA	GTATCCCCAG
1260	TACTCACAAC	CAATAATAGT	CTGTACCCTT	TTTCCGCAGT	TTTATTTGGA	GAAAATATCA
1200	AGGTTTGTGG	AGCCAGAAAA	TATGTAAAAG	CCTGGGAGGA	GAACAACTTA	CGGCGCTTAA
1140	AGAGTATAAA	CTGATGAGGA	CCGAACAAAC	TGAACTTGCA	ACGCGAGGAA	AGGGTGGCAT
1080	GTATCTTTTA	TCGTGGAGTG	ACCGGCAACC	GAGATCAAGC	GGGACGTCTC	CAAAGTGTAT
1020	GCTGATAGGT	AGCTGGCAAA	ATTCTTCCCC ATGGAAGCTG	ATTCTTCCCC	TCGGGAAGGA	ACGIATGAGC

54 108 162 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCT AGA //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC TGA

Figure 17P

Deep Vent- (HMf-like) DNA polymerase fusion protein [Fig.17-P]

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 63)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG (ALL POSSIBLE CODONS FOR ARGININE) 9 120 ATGATACTIG ACGCIGACTA CATCACCGAG GAIGGGAAGC CGATTATAAG GATTITCAAG AAAGAAAACG GCGAGITIAA GGIIGAGIAC GACAGAAACT IIAGACCIIA CAITIACGCI V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

00	0.6	~ <i>(</i>	0 0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80
18(300	360	42(54(90	099	720	780	840	900	960	1020	1080	1140	1200	1260	132(138(144	1500	156	162	168	174(1800	186	192	198	204	210	216	222	228	232
GAGGCATGGG	GGATAAGATA	GAAGAGGTAC	GCTCGCATTT TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	TAACGTCTCA	GGTTGGGCAC	ATTGGATGAA	GAAGATGCTT	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA	GCTTGAGTAC	GATAGATGAG	CGAAATAGCC	TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAAG	
TAACCGCCGA O	_		AGCTCAAGTT C AGGGGCCCAT 1		TCCTCAAGGT (TCGACCTTCC (GGGACGGTAG	GAAGGATACA (CCCTCGAGGC 1	AGATAGCTGA (AGGATGCAAA (CAAGGTTAGT (AGTGGTACCT (AGAGGGAGTA (AGAAAGGGCT (TAATCACCCA 1	TCGCCCCAGA (TCAAGAGGTT 1	CAATCGAGAA (ATTATGGGTA :	TTACGGCCTG (GGTTCAAAGT (CCGAGGAGAT 1	Ξ.	AGTATGCGTT (ATGGCAACGT :	ACGAAATACC :	ACAAGGCTAT 1	TGAGGCCTGG (GGGCTATCCT	TAGAAAATCA (AAGACCTCAG (AGAAG //
GTTAGGAAGA GTAAGGAAGA	CAGGACXXXC	GAGTACGACA	GAGGATGAAG	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGCCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
GATTGATGAG TGCCGAAAAG	TGAACACCCT	TGACATCTTT	TCCAATGGAA	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GTTCTTCGTG	GGGCCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
ATGACTCGCA GAATTATAGA	GGCTGTACTT	CCGCAGTTAT	AAGGCCTAAT	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC
CTCCTCAAAG AAGATAGTGA	GAGGTATGGA	AGAGAGCATT	GACATAGACA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGCCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

54 108 162

Figure 170

(HMflike) - Deep Vent DNA polymerase fusion protein [Fig.17-Q]

// Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 37) Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 63)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

108 162 GAG GAA GCA GGT AGA GGT GCT AGA AAG CAC CTT CAC ATA GAG AAG AGC GAT CTT GCA GAC AGA CTT GCA ATT AAG GAG CAA GCA GCT AAG GTA CTT GCA ATT GCC CCA GTT GCA AAA AAG GCA GTA GAA GAC ATT AAG CTC CCA TTA GTC AGA GIT AGC ATC GAG GAA GTT AAG ATT GGA GCT CAG ACC //ATG ATG AAA GCT AAG

9 99 720 780 240 300 360 420 480 540 600 840 900 960 1020 1080 1140 1200 1260 1320 /ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT TGAGCCAAAG GAGGCATGGG GAGGCCGATT GGATAAGATA GAAGAGGTAC GCTCGCATTT TATAATGATA TCTCCCGTAC GATAAGGGAG CTTTGACCTC AGTTTATGAG GGCCTGGGAG GGTAACGTAC CGGCCAGCCC CCTCAGGAAG CGAGAGAAGG GGTTGGGCAC CTATCTAGTI GATTGATGAG GTTAGGAAGA TAACCGCCGA AAAAGATCGA TCGCCCCAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG CCGCAATAAG AGGGCCCCAT TCCTCAAGGT GGGACGGTAG GAAGGATACA CCCTCGAGGC AGATAGCTGA CAAGGTTAGT TAATCACCCA TTCCGTTCGC TCGACCTTCC AGGATGCAAA AGTGGTACCT AGAGGGAGTA GGCGATGAAG AGCTCAAGTT AGAAAGGGCT AGCCAAAGTC ATAACGTGGA AAGCCGGATG AAGGAGCCGG GAATACGATG GAGTTCGCGA TACGCTCACG TATTCAATGG AACTTGGTGG CAGGACXXXC GAGTACGACA ATAAAGCGGT GAGATAAAGG CCAACATACA CCCTCGATAA GGCGATTCTT GCCCAGCTTT CCCCTGGGAA GAGGGAGATG GGCTCCAAAC GGGATACGTT AGGGTGTAGG TGAACACCCT TGACATCTTT TCCAATGGAA CGAAGGGGAG GACAGCGGTG AGTTGCAAAG CCCAATGGAG TTCAACTGGC GAGCCTGTAC TACCTACAAC GATAAAGCTA GGAGAAAGTT GATAAACCTC TGAACAGGGA AAGGCCTAAT TTTCTAGGTC ATGACTCGCA GAATTATAGA GGCTGTACTT ATGAGGAAGA AAAAGCTCGG TTGGGGATAT GAAAGCCAAA GACTGGAGAG TAGATTTCAG CCGCAGTTAT TTTCCAGCGA ATGTTATAAT GGGAGTTCTT GCTACGCTGG CCCTCTATCA TTAGGAGAAC GGAATGAATT CTCCTCAAAG CCGGATACGC CTGTGGGATG CTAAGGGAGA GAGGTATGGA CTAATAGACA AGCTATGCTG AAAGATCCCG AAGAGGCCG ATGCAGAGGC TACCACGTGA GCAATCTTCG GCCTACGAGA TTAGTTTCCC AAGATAGTGA GTCGAGGTAG ACTGGAAAGG GAGCTCGGTA AGAGAGCATT GACATAGAAA

AAGTTCTGCA	AGGACTTCCC	AAGTICIGCA AGGACTICCC GGGGTITAIC CCCAGCCTGC ICAAGAGGIT AITGGAIGAA	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
AGGCAAGAAA	TAAAAAGGAA	AGGCAAGAAA TAAAAAGGAA GATGAAAGCT TCTAAAGACC	TCTAAAGACC	CAATCGAGAA GAAGATGCTT	GAAGATGCTT	1440
GATTACAGGC	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
GCAAAAGCCC	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
TATATAGAGT		TCGTAAGGAA GGAACTGGAG GAAAAGTTCG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
GACACAGATG	GACTCTACGC	GACACAGATG GACTCTACGC CACAATTCCT GGGGCAAAAC CCGAGGAGAT AAAGAAGAAA	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
GCCCTAGAGT	TCGTAGATTA	SCCCTAGAGT TCGTAGATTA TATAAACGCC AAGCTCCCAG GGCTGTTGGA GCTTGAGTAC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
GAGGGCTTCT		ACGTGAGAGG GTTCTTCGTG ACGAAGAAGA AGTATGCGTT	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
GAAGGGAAGA	TAATCACTAG	TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
AAAGAAACCC	AAGCAAAAGT	AAGCAAAAGT CCTAGAGGCT ATCCTAAAGC ATGGCAACGT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
GTAAAGATAG		TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
CTAGTTATTT		ACGAGCAGAT CACGAGGCCC	CTTCACGAGT	CTTCACGAGT ACAAGGCTAT AGGTCCGCAC	AGGTCCGCAC	2040
GTTGCCGTGG	CAAAAAGGTT	AGCCGCTAGA	AGCCGCTAGA GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
GGGTACATAG	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	AGACGGGCCA ATAAGCAAGA GGGCTATCCT	TGCAGAGGAG	2160
TTCGATCTCA	GGAAGCATAA	GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
GCCGTTCTTA	GAATATTAGA	GCCGTTCTTA GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
ACTAAACAGA	CAGGTCTTAC	ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG TAA	AACATCAAGA	AGAAG TAA		2328

Figure 17R

JDF-3 - (HMf-like) fusion protein [Fig.17-R]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 63) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93B MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTC<mark>GAG</mark>ATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAA CAGGICTGIGGAGGICTGGGICCTCTACTICACGCACCCGCAGGAC<u>XXX</u>CCGGCAAICCGCGACAAAIAAGGAAGCACCCCGCGGTCAICGACAICTACGAGIACGACAIACC acgecegnegetacetreaggagecegagergegacretreggacaararatergrataretragacrrrregragetereradecriteaareararecaecaaaaegec ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGAGGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGCCGAGGGGCCTTGAGAG GGTCGCGCGCTACTCGATGGAGGCGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGA ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAA ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT

CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCGC cagaagataaagagaagatgaaggcaactctcgacccgctggagaaatctcctcgattacaggcaacgdGcCatcaagattctcgccaacagctactacggctactacggct ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCCGAGAGCGTTACGGCATGGGGAAGGGAATTACATTGGAAATGGTCATCAGAGAGGCTTGAGGAAAAGTTCGGTTTTAAAGTCCT CTATGCAGACACAGACGGTCTCCATGCCCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATTCAATCCCAAACTGCCCGGCCTTCTC actggagcgagatagcgaagcgaagcgagggttttggaggcgatactcaggcacgtgacgttgaagaggccgtcagaattgtcagggaagtcaccgaaaagctgagcaaa GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGGTCTAAGGACTACAAGGCCACGGCCCGCACGTAGCCATAGCGAAgcGTTTGGCCGCCAGAGGT GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

108 162 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT AAG ACC GIT AAG GIC GAA GAC AIT AAG CIC GCA AIT AAG AGC IGA

Figure 17S

(HMf-like) - JDF-3 fusion protein [Fig.17-S]

// Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 63) // Nucleotide sequence (SEQ ID NO: 39) Nucleotide sequence (SEQ ID NO: 63) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 162 GCT CAG AGA GTT AGC GAG CAA GCA GCT AAG GTA CTT GCA GAG CAC CTT GAG GAA AAA GCT ATT GAG ATC GCA AAA AAG GCA GTA GAT CTT GCA AAG CAC GCA GGT AGA AAG ACC GTT AAG GTC GAA GAC ATT AAG CTC GCA ATT AAG AGC // //ATG ATG GGA GAA TTA CCA ATT GCC CCA GTT GAC AGA CTT ATA AGA AAG GCT GGT

TCGACATCTACGAGTACGACATACCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAGGAGGTTAAAGCTTAAAACTCATGTCCTTQGAQATC //ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAG GTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAA gaagaaaagttcctcggcaggtctgggaggtctgggtcctctacttcacgcacccgcaggac**xxx**ccggcaatccgcgacaaaataaggaagcacccgggggtca TCCTTACGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGGTCGTTAAGGAGAAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACT GCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACG CCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAGATAACCGCGGGGGGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGT

AAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCTA CTGCCCGGCCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGGCAAGATAACCACGCG GGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTJTCAATCATCATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGT CGGGCTTGAGATAGTCAGGCGCGACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAA TTGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGGGGAGCTCAAGGACTACAAGGCCACCGGC CCGCACGTAGCCATAGCGAAGCGTTTGGCCGCCAGAGGTGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAG **GGCGATTCCCTTCGACGAGGACCCGACGAAGCACAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCG** GTAGGAGCTACGACGTTGCCCCCGAGGTCGGTCACAAGGTCTTCTGCAAGGACTTCCCGGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAGATA TGCCAGGGCAAGATGCTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAGTTCGGTTTTA AAGTCCTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAA AGCTTGGCAGGGAGTTCTTCCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTTC GCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGA

Figure 177

Pyrococcus furiosus DSM 3638, Archeael hostone (HMf-1) section 85 of 173 of the complete genome. 'product="pcna sliding clamp (proliferating-cell nuclear antigen)" ACCESSION No: AE010210 REGION: complement (8333..9082) [Fig.17-T]

Nucleotide sequence (SEQ ID NO: 67) Amino acid sequence (SEQ ID NO: 68)

90 270 108 324 126 378 144 36 108 54 162 72 162 486 GAC ATA CCG N AAC I ATA ACA ССА A GCT н GCA CTC D GAT GAA ATA ggg CIC V GTT L TTA Ö D T GAC ACC ' GAC GAT N AAT I A R ATT GCC AGG CHI g GGA T ACT V L K GTC CTA AAA Ы Д g GGA V GTT I ATT CAA GAA $_{
m L}$ Ø 闰 T ACA CA O GAA T ACA GAC K AAG ø FTTT E M GAG ATG GAA gca Gca GAA GTT I ATT I ATT TTT > L G CTT GGA E I T GAG ATA ACA D S I K GAC AGC ATA AAA CŢĠ CCA GAG AAA AAA AAA ы ¥ g GGT AAA TTTV GTC E GAA × [z, V GTA GTT GCA gcg V GTT GTT r Aga > > ø gcc Gcc AAG TTA GAT GTA GGT R AGA GTT > Д Ω > ര V S GTG AGT (CIA I ATA TTC GTT GAG S AGT GAA TTT GAA 臼 ഥ > 团 ш I ATC GAT ССА TAT N AAC L CTA K AAG × ഥ Ω GTA K AAG GCC CCC GCA CTA ATA D GAT K AAA GAA ы 团 > H A S GCC TCT SAGC K ATC TTA M ATG GAG GTT TACT 臼 Ы > Н GAA CTA AAG **₽** $_{
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ATA	ACA	AAG	TAT	GAG
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V	E	L	M	V
GTT	GAG		ATG	GTT
E GAA	CAA	G GGA	CAA	r Aga
Q	V	K	M	P
CAG	GTT	AAA	ATG	CCA
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E	I	M	M	L
	ATC	ATG	ATG	CTG
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F	E	GGA	T ACA	E GAA
E	L	Y	V	D
	CTT	TAT	GTT	GAT

Figure 17U

(PCNA)-Taq DNA polymerase fusion protein [Fig.17-U]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 65) Amino acid sequence (SEQ ID NO: 68) // Amino acid sequence (SEQ ID NO: 66)

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TAA H

Taq DNA polymerase- (PCNA) fusion protein [Fig.17-V]

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 68) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 67)

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×	TAT	>	GTT	Д	GAT

Figure 17W

Pfu DNA Polymerase (WT) -(PCNA) fusion protein [Fig.17-W]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 67)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat caactctaca cetecectat tttetetett atgagatttt taagtatagt tatagagaag gttttatact ccaaactgag ttagtagata tgtgggggagc ataatgattt tagatgtgga taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga gtagaagcgg

54 108 1162 216 2216 2270 2324 432 432 4432 702 702 CCG AAC ATA ACA GCT AAT ACT GCA GCA GGG GTT TTA GCA CIC GAT GAA CTA AGC GAT ATT CTC GAT AAG ပ္ပင္ပ AAT GGA ACC GAC AGG AAG ACT AAA GAA CTA ATT CTA GAC GGA GTT ATA ACA AAG GAG GAG GGA GAC ACA GTC ACA CAA GAA GAA GTT ATT GAA GCA ATT ATG TTT GTT GAG CII ATG AAA CIG AAA ACA GAG AAA GAA CAA CCA GGA GGA AAA TTT ATA GGT ATA CAG GTC GAA GAA CTT GTT GCA gcg GTT GTT AGA GAG GTA GTT AGC ACC GAG GTT CCC GGT AAG TTA GAC GAA gcc AGA GTT GAT GTA ATC ATG ATG CTA GAA AGT AGT GAC GAG GAA TIC GGA ATA GTT $_{
m LLL}$ GAT CCA TAT ATC AAC CTA AAG GTG GAG TTG TCC GTA ATA TTA GAT AAA AAG GAA CC CTA GCA CIC GGA GCA TTA AAG AAG ATG AGC GAG ACT TCT GGA TAT GTT GCC AAG TTTCTA GGA TIC gcc ATG AGC AGA GAG AGG GAT ATA AGT AAA GAT GTC ATA CAC TTTCCA $_{
m LLL}$ CCA GCA AGC ACA ATG GAC ACA AAA TTT GAA GGA CTC AAG CTT AGC TCA ATG AGA GAA GTT GAA ACC TAT

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tgttcttgg

aagattgaga

Figure 17X

(PCNA) - Pfu DNA Polymerase (WT) fusion protein [Fig.17-X]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 61)

ATG CCA TTT GAA AI	ATC GTA	TTT 1	GAA	GGT	GCA	AAA	GAG	TTT	CCC	CAA	CTT	ATA	GAC	54
GCA AGT AAG		_	GAG	ggg		TTT	AAA	GTT	ACA (GAA	GAT	GGG	ATA	108
ATG AGG GCC	ATG GAT	CCA	AGT	AGA	GTT	GTC	CTG	ATT	GAC	CTA	AAT	CIC	CCG	162
TCA AGC ATA TTT AG	AGC AAA	TAT	GAA	GLL	GTT	GAA	CCA	GAA	ACA	ATT	GGA	GTT	AAC	216
ATG GAC CAC CTA AA		; ATC	CTA	AAG	AGA	GGT	AAA	GCA	AAG (GAC	ACC	TTA	ATA	270
CTC AAG AAA GGA GAG	G GAA	AAC	TTC	TTA	GAG	ATA	ACA	ATT	CAA	GGA	ACT	GCA	ACA	324
AGA ACA TTT AGA GI	GTT CCC	CTA	ATA	GAT	GTA	GAA	GAG	ATG			GAC	CIC	CCA	378
TTC	T GCA	AAG	GTT	GTA	GTT	CTT	GGA	GAA		CTA	AAA	GAT	GCT	432
AAA GAT GCC		GTG	AGT	GAC		ATA	AAA	TTT	ATT (AGG	GAA	AAT	486
GAA TTT ATA ATG AA	AAG GCA	GAG	GGA	GAA	ACC	CAG	GAA	GTT	GAG	ATA	AAG	CTA	ACT	540
GAA GAT GAG	GGA TTA	TTG	GAC	ATC	GAG	GTT	CAA	GAG	GAG	ACA	AAG	AGC	GCA	594
GGA GTC AGC	TAT CTC	TCC	GAC	ATG	GTT	AAA	GGA	CTT	GGA	AAG	ggg	GAT	GAA	648
GTT ACA ATA AAG TI	LTT GGA	AAT	GAA	ATG	CCC	ATG	CAA	ATG	GAG '	TAT	TAC	ATT	AGA	702
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ccctggtcct gggtccacat		atatgttctt		actcgccttt	cttt		atgaagaatc	atc	cccagtcgc	agto	gc			
tctaacctgg gttatagtga		caaatcttcc		tccaccaccg	accg		cccaagaagg	agg	ttatttctat	ttct	at			
caactctaca cctcccctat		tttctctctt		atgagattt	ttt		taagtatagt	agt	tatagagaag	gaga	ag			
gttttatact ccaaactgag		ttagtagata		tgtggggagc	gagc		ataatgattt		tagatgtgga	tgtg	ga			
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taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc

Figure 17Y

(PCNA) - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-Y]

// Nucleotide sequence (SEQ ID NO: 27) //Nucleotide sequence (SEQ ID NO: 28) Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 67) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA,

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                                                                                                                                                                                                                                CCTCTACATT
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                                                                                                                                                                                                                                                                                                                             AGGTCCTCAC
                                                                                                                                                                                                                                                                                                                                                       AGCTGAGGAA
                                                                                                                                                                                                                                                                                                                                                                     GGTTCTTCCA
TATCAGGGAG
             ATATTAGCG
                                                     TGTATATGAA
                                                                               GGCAACTTAT
                                                                                                                                                CAATGTTTCT
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                          CGAGCCCAAG
                                        TTTCGACTTG
                                                                                                         ACTTAGGAAA
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            GGAGACTCAT TCGCATTCCC
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TTCTCAGGAT
                         GAGATGGAAG
                                                   CACTAGAGGC
                                                                  AGATAGCAAA
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                                                                                                                      AAGAGGAGTA
                                                                                                                                                             TCGCTCCTCA
                                                                                                                                                                                                      TCTACGGATA
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                                        GAAGAATACA
                                                                                            CAAGATTAGT
                                                                                                                                   AAAAGGGGTT
                                                                                                                                                 TAATTACCCA
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                                                                                                                     AAGCCAAGTG
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ATAAAGAGAT
                                                                 TACGCCGACG
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                                                                               TACTCGATGG
                                                                                                         AACCTTGTAG
                                                                                                                                   AAAGAGCCAG
                                                                                                                                                              AACTATGATA
                                                                                                                                                                            CCAAGTCTCT
                                                                                                                                                                                        ACTCAAGATC
                                                                                                                                                                                                      GCAAATTCTT
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                                                                                                                                                                                                                                                                                     ATAGTTAGGA
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                                                                                                                                                                                                                                                                                                                                           GGAGTTAAAA
                                                                                                                                                                                                                                                                                                                                                                    GAATATTACA
                           ACCATTGGAA
                                                    CCAACATACA
                                                                                           ATTCAGCTTT
                                                                                                                                                 CCCTCGATTA
                                                                                                                                                                                                                    GCTGAGAGCG
                                                                                                                                                                                                                                              GGAGGAGAAA
                                                                                                                                                                                                                                                           AAGCTCCCTG
                                        GAAGTCAAGG
                                                                                                                                                                                                                                                                        ACGAAGAAGA
                                                                                                                                                                                                                                                                                                                                                        ATTAGCAATA
                                                                                                                                                                                                                                                                                                                                                       CGATGGTCCA
GAGAGAGATG
             TACTTATAAT
                           GATTAAATTA
                                                                                            TCCAATGGAA
                                                                                                                                   TGGATTCGTT
                                                                                                                                                              GGGATGCAAG
                                                                                                                                                                                         AATGAAGGAA
                                                                                                                                                                                                                                                           CATAAATTCA
                                                                                                                                                                                                                                                                                                  TTTGGAGACA
                                        GACGGCTGTA
                                                    AATAAATCTC
                                                                   GGAGAAGGTA
                                                                                AGTTGCCAAA
                                                                                                         AAGCACAGGG
                                                                                                                      AGCTCCAAAC
                                                                                                                                                                            TGGTTTTATA
                                                                                                                                                                                                                                                                        ATTCTTCGTT
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                                                                                                                                                                                                       AAAACTCTTA
                                                                                                                                                                                                                                GGAGCTCGAA
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             ACATTATAGT
                           AAAAACTTGG
                                                                                                                                                 TAGATTTAG
                                                                                                                                                                                                                                TAGTATGGAA
                                                                                                                                                                                                                                              GTCTCTATGC
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                                                                                                                                                                                                                                                                                                                                           CAAAGAAACT
                                                     TAACAAGGAC
                                                                                ACCTTGAGAG
                                                                                                                                   GCTACACAGG
                                                                                                                                                              TAAATCTTGA
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                                                                                                                                                                                                       AAAAAGCGAT
                                                                                                                                                                                                                                                                                                  AAGCTAGAGT
                                                                                                                                                                                                                                                                                                                TAAAAGAAGT
TATCAAGCGA
                                        TAGGCGATAT
                                                                  GAAAGCCAAA
                                                                                            AAGAATTCCT
                                                                                                          TTTCAAGGTC
                                                                                                                      GAAACGAAGT
                                                                                                                                                                            AGGACATCCC
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                                                                                                                                                                                                                                                                                                                                                                      AAAAGCACAA
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             AAGGATCCTG
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                         AAAAGGGCAG
 GTTGAGGTTG
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                                                                                AGTGGAGAGA
                                                                                             GAACTCGGGA
                                                                                                        TTATGGGATG
                                                                                                                                   CTCAGGGAGA
                                                                                                                                                 ATAGTATACC
                                                                                                                                                                                                                                TACATCGAGT
                                                                                                                                                                                                                                              GACACTGATG
                                                                                                                                                                                                                                                                         GAAGGGTTTT
                                                                                                                                                                                                                                                                                      GAAGGAAAAG
                                                                                                                                                                                                                                                                                                  AAAGAAACTC
                                                                                                                                                                                                                                                                                                                                            GTAGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                   GCGCTACTTA
                                        ATGCAGAGAA
                                                     TATCATGTAA
                                                                  GCAATTTTG
                                                                                                                       GCCTACGAAA
                                                                                                                                                               CCCGATACTC
                                                                                                                                                                             AAGTTCTGCA
                                                                                                                                                                                          AGACAAAAGA
                                                                                                                                                                                                                    GCAAAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                              // TGA
```

Figure 17Z

PPU DNA POLYMERASE (V93 R OR E) - (PCNA) fusion protein [Fig.17-Z]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1440 1020 1080 1140 1200 1260 1380 1320 1500 1560 009 999 720 840 006 960 420 480 540 ATTCTTCGTT ACGAAGAGA GGTATGCAGT AATAGATGAA CAATGTTTCT GGGAAGAAAG GCTTGAATAT CTGTTATTAG GCTATTCAAA TAACGGGGGA AAGGCATGGA AGCTAAAGAT TCTTGCCTTC AAGGCCCAAT TATAATGATT TGGACAACCT ACTTAGGAAA TCAAAGAAGG AGTAGGCCAC GTTAGAGGAA AATACTCCTT TTATGGCTAT CCTCTACATT AAAGAAAAG TTAGACCATA CATTTACGCT CAAGCCTATT AGAAAAGTT AAAGAGATAC TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG TTTCGACTTG TGTATATGAA AGCCTGGGAA GGCAACTTAT GTGGGAAAAC GLUTAMIC ACID) AGTTTCTCGG CCACTATTAG TTCCATTTGC AAAACATAGA GAAGAATACA CACTAGAGGC AGTTGCCAAA TACTCGATGG AAGATGCAAA CAAGATTAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TAATTACCCA TCGCTCCTCA CTATAGAAAA TTACTGCCTG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT GACTGCTAGA TTCTCAGGAT TCGCATTCCC GAGATGGAAG AGATAGCAAA AAGCACAGGG AACCTTGTAG AGTGGTTCTT AAAAGGGGTT TGGGACATTT TCTACGGATA GATTTAAAGT AGCAAAGGTG ATTACTTGGA CCCTCGATTA GCTGAGAGCG CATAAATTCA AAGCTCCCTG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GAATACGATA GGGGAAGAAG GAGTTTGGAA GAGAGATG ATAAAGAGAT GGAGACTCAT GACGGCTGTA GAAGTCAAGG CCAACATACA TACGCCGACG TCCAATGGAA ATTCAGCTTT AAAGAGCCAG AACTATGATA ACTCAAGATC GCAAATTCTT GAAAAGTTTG V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GAAGGAAAAC GATAGAACTT GATTGAAGAA GTTAAGAAAA TGTAGAGAG GTTGAGAAAA CAAGATXXXC ACCATTGGAA CCAAGTCTCT TGGTTTTATA AATGAAGGAA GGGATGCAAG AGCCCTATAT AAAACTCTTA TAAGGAGTGT ATGATTTTAG ATGTGGATTA CATAACTGAA GATAGAGCAT GATTAAATTA AATAAATCTC GGAGAAGGTA TGGATTCGTT GGAGCTCGAA GGAACATCCC GGACATCTTC CGAAGGAGAA TACTTATAAT ACCAATGGAG GAAGGGTTTT ATAAGAGGGG TAGATTTTAG AGGACATCCC TTAAGACAAA AAAAAGCGAT TTGTAAAATA TTTCAAGGTC GATGGTACTG GAAAATTTAA CTTCTCAGGG ATGATTCAAA GAATTGTTGA CAGCAGTIGI AAGGCCTAAT CCCTCTATCA ATGAAAATGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA ACCTTGAGAG AAGAATTCCT GAAACGAAGT GCTACACAGG TAAATCTTGA TAGTATGGAA AACTTTATT TATCAAGCGA GCTCTAGAAT ACCGTGTGGA CCCGATACTC AAGTTCTGCA AGACAAAAGA GACTATAGAC GACACTGATG AAAGAGAACG AAGATTGTGA AGAGAACATC AGTTATGCAG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA AGTGGAGAGA GAACTCGGGA GCCTACGAAA CTCAGGGAGA ATAGTATACC GCAAAAGCAA TACATCGAGT CTCATCGACA GATATAGAAA GTTGAGGTTG GCAATTTTTG TTATGGGATG

216 270 486 540 324 378 432 648 108 162 594 AAC AAT GAA ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA ATA ACA CCA GCT ACT GCA ATG CCA TIT GAA ATC GTA TIT GAA GGT GCA AAA GAG TIT GCC CAA CIT ATA GAC CIC GTT TTA GCA GAT TAC ATT GAT GAA CIC CTA AGC GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 2040 2100 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220 GCGCTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860 CTA AAT ACC GGA AGG AAG ACA AAG TGA GGA ACT GTT GAC CTA AAA AAG GCC CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC ATT TAT ggg ACA GAA GTC CTG ATT GAC AAG GAG GGA GAG CAA GAA GIC ATT GAG GAA CCA GAA GCA GAA GTT GAG ATG $_{
m LLL}$ GAG CTIATA ACA ATT GTT CAA ATG ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GGA GGT AAA GGA CAA ATA AAA GAA GAA CAG CTT GTT AAA CCA AGT AGA GTT GIT AGA GAG S GCT GTA AGC ACC GAG GTT GTT GAT GAC GAA CTA AAG TTA GTA ATC ATG GAA GTT GAC ATG GAA ATA AGI TAT ATC AAC CTA AAT AAG AAG AGC ATG AGG GCC ATG GAT ATA TTT AGC AAA CCC GGA ACA CIC GAA GCA GCA CTA AAG GAG GTT ACT AAG TAT LLL TCT GGA AAG GGA AGA GAG CAC GIC ATA $_{
m LLL}$ AAA CCA GAT ATA GAT TCA AGC GIT ACA CTCGCAATAT GTAGCTGTTG $_{
m LLL}$ GIT AAA TAT GGA CTC AAG AGA ACA GAA CTT ATG GAC CTT GAA GAA

Figure 17AA

PFU DNA POLYMERASE (G387P/V93R OR E)-(PCNA) fusion protein [Fig.17-AA]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 ATGATITIAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 G387P Mutant (CCN is the codon for Proline where $N=C,\ G,\ A,\ or\ T)$ V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

	108	162	216	270	324	378	432	486	540	594	648	702	
GAC													
ATA	ATA	CCG	AAC	ATA	ACA	CCA	gCT	AAT	ACT	GCA	GAA	AGA	
CTT	GGG	CIC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
CAA	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ggg	TAC	TGA
300			ATT	GAC		GTT	CTA		ATA	ACA	AAG	TAT	GAG
rtt G	ACA			AAG					GAG	GAG	GGA	GAG	GAA
GAG T				GCA					GTT	GAG	CLT	ATG	GTT
AAA G		CTG						AAA	GAA	CAA	GGA	CAA	AGA
GCA A								ATA		GTT	AAA	ATG	CCA
GGT G								AGC		GAG	GTT	င္ပင္ပ	GCT
GAA G	ggg	AGA	GTT						GAA	ATC	ATG	ATG	CIG
TTT G	GAG	AGT	GAA	CTA	TIC	ATA	$_{ m GTT}$	AGT	GGA	GAC	GAC	GAA	CTA
GTA 1	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GTG	GAG	TTG	TCC	AAT	$_{ m TIC}$
ATC G	ATA	GAT	AAA	AAG	GAA	ပ္ပင္ပ	GCA	CTA	GCA	TTA	CTC	GGA	ACA
3AA A	TTA	ATG	AGC	AAG	GAG	GTT	ACT	$_{\rm ICI}$	AAG	GGA	TAT	$_{ m TTT}$	CTT
LTT C	AAG	gcc	$_{ m TTT}$	CTA	GGA	AGA	TTC	ggg	ATG	GAG	AGC	AAG	AGA
CCA T	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
ATG C	GCA	ATG		GAC						GAA	GGA	ACA	GAA
// A									GAA	CLT	TAT	GTT	

54

Figure 17BB

(PCNA) - PFU DNA POLYMERASE (G387P/V93R OR E) fusion protein [Fig.17-BB]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 30) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 29)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)
V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432
	ATA	CCG	AAC	ATA	ACA	CCA	GCT
GAC	GGG	CIC	GTT	TTA	GCA	CIC	GAT
ATA	GAT	AAT	GGA	ACC	ACT	GAC	AAA
CIL	GAA	CTA	ATT	GAC	GGA	GTT	CTA
CAA	ACA	GAC	ACA	AAG	CAA	GAA	
CCC	GLT	ATT	GAA	GCA	ATT	ATG	GAA
TTT				AAA		GAG	
GAG	TTT	GTC	GAA	GGT		GAA	
AAA	gcg	GTT	GTT	AGA	GAG	GTA	GTT
GCA				AAG			
GGT						ATA	GTT
GAA						CTA	
TLL	ATA					CCC	
GTA	TTA	ATG	AGC	AAG	GAG	GTT	ACT
ATC	AAG	ggg	$_{ m LLL}$	CTA	GGA	AGA	TIC
GAA	AGT					TTT	CCA
TTT	GCA	ATG	AGC	GAC	AAG	ACA	CTT
ATG CCA	ACC	AGC				AGA	

594 648 540 702 486 GCA GAA AGA ACT AAT ATT GAA CTA GAT AGC TAC AAG ggg AGG AAG TAT ATA ACA AAG GAG GAG GGA GAG ATT TTTGTT GAG ATG CTT CAA AAA GAA CAA GGA ATA CAG ATG AAA GTT CCC AGC GAG GTT ACC GAC GAA ATG ATC ATG GGA GAC GAA AGT GAC GTG GAG TTG AAT TCC GGA CTA GCA TTA CIC $_{
m TCT}$ AAG GGA TAT TTTATG AAG AGC GAG ATA GAT ATA GAT GTC ACA AAA TTT GAA GGA GTT GAA CTT TAT

1020 1260 1320 1380 1440 1500 1560 1620 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 1140 1200 1080 9 780 840 900 960 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 TGGACAACCT TGAAATTGCA CAAGCCTATT GGCAACTTAT ACTTAGGAAA TCAAAGAAGG CAATGTTTCT AGTAGGCCAC GGGAAGAAAG AATAGATGAA AGAAAAGTT TCTTGCCTTC TATAATGATT ATATTAGCG CGAGCCCAAG TTTCGACTTG AGCCTGGGAA GTGGGAAAAC GTTAGAGGAA AATACTCCTT TTATGGCTAT GCTTGAATAT AAAGAGATAC TCTTCCATAC TATCAGGGAG CCTCTACATT AAAGAAAAG GAG // TGTATATGAA GAA GAGATTGGAG TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG AGCTAAAGAT AACCTTGTAG AGTGGTTCTT AAGAGGAGTA TTACTGCCTG GGTATGCAGT GTT CCACTATTAG TTCCATTTGC AAGGCCCAAT AAAACATAGA TCGCATTCCC GAGATGGAAG GAAGAATACA CACTAGAGGC AGATAGCAAA AAGATGCAAA CAAGATTAGT TCGCTCCTCA CTATAGAAAA TTCTCAGGAT TAATTACCCA TGGGACATTT TCTACGGATA GTGAGGAAAT GACTGCTAGA AAAAGGGGTT GATTTAAAGT CCA AGA GAATACGATA GGGGAAGAAG GAGTTTGGAA ATTACTTGGA TACTCGATGG AAGCCAAGTG AAAGAGCCAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA CAAGATXXXC GGAGACTCAT ATTCAGCTTT CCCTCGATTA AACTATGATA AAGCTCCCTG GAAGTCAAGG CCAACATACA TACGCCGACG GCTGAGAGCG GAAAAGTTTG ATAAAGAGAT ACCATTGGAA ACTCAAGATC ACGAAGAAGA CCAAGICICT GCAAATTCTT GGAGGAGAAA GCT CTA CTG AAGCACAGGG AGCTCCAAAC GGGATGCAAG GGACATCTTC ACCAATGGAG AGCAAAGGTG GACGGCTGTA TCCAATGGAA AGCCCTATAT CATAAATTCA ATTCTTCGTT GGAACATCCC CGAAGGAGAA GAGAGAGATG TACTTATAAT GATTAAATTA GGAGAAGGTA AGTTGCCAAA NGGATTCGTT TGGTTTTATA AATGAAGGAA TAAGGAGTGT GGAGCTCGAA AACTATCCCA AATAAATCTC AAAACTCTTA TIC ACA CŢŢ GAATTGTTGA AACTTTATTT CAGCAGTTGT TAACAAGGAC ACCTTGAGAG AAGAATTCCT GTCTCTATGC AAGGCCTAAT ATGAAAATGA TAGGCGATAT TTTCAAGGTC TTAAGACAAA AAAAGCGAT GATGGTACTG TTGTAAAATA ATAAGAGGGG CCCTCTATCA TATCAAGCGA ACATTATAGT AAAAACTTGG GAAAGCCAAA GAAACGAAGT AGGACATCCC TAGTATGGAA GCTACACACC TAGATTTTAG TAAATCTTGA AGA GGA GAAGGAAAG AAGATTGTGA ACCGTGTGGA SAAGGGTTTT GAA AGTTATGCAG GTTGAGGTTG AAAAGGGCAG AGTGGAGAGA GAACTCGGGA TTATGGGATG CTCAGGGAGA ATAGTATACC CCCGATACTC AAGTTCTGCA GACTATAGAC GACACTGATG GCTCTAGAAT CTCATCGACA GATATAGAAA AAGGATCCTG ATGCAGAGAA TATCATGTAA GCCTACGAAA AGACAAAAGA AGAGAACATC GCAATTTTTG GCAAAAGCAA TACATCGAGT GAT

2100 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980 AAAGAAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920 AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040 GGGCAATTCT AGCTGAGGAA 2160 TGGAGAACCA GGTTCTTCCA 2220 GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 TAAAGCCAGG AATGGTAATT ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //TAG AGCTGCTAAA GGAGTTAAAA ATTAGCAATA GAATATTACA CGATGGTCCA GTATGACGCA ATGAGCAGAT GGATATTGGA CAAAGAAACT TACTTAGAGG AAAAGCACAA CTCGCAATAT GGATACATAG TACGATCCCA GCGGTACTTA GTAGCTGTTG

Figure 17CC

(PCNA) -PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein [Fig.17-

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 31) Nucleotide seguence (SEQ ID NO: 67) // Nucleotide seguence (SEQ ID NO: 32)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where $N=C,\ G,\ A,\ or\ T)$ V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
GAC	ggg	CIC	GLT	TTA	GCA	CIC	GAT	GAA	CIA	AGC	GAT	ATT	
ATA	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ည္သ	TAC	\
CIT	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ညည	ATA	ACA	AAG	TAT	GAG
CAA	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
CCC	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TTT	GTT	GAG	CTT	ATG	GTT
TTT:	AAA	CIG	CCA	AAA	ACA	GAG	GGA	AAA	GAA	CAA	GGA	CAA	AGA
GAG	TTT	GIC	GAA	GGT	ATA	GAA	CTT	ATA	CAG	GTT	AAA	ATG	CCA
AAA	gcg	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
GCA	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
✓ GGT	GAG	AGT	GAA	CTA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
GAA	GAT	CCA	TAT	ATC	AAC	CTA	AAG	$_{ m GTG}$	GAG	TTG	\mathbf{I}^{CC}	AAT	TIC
\ TTT	ATA	GAT	AAA	AAG	GAA	CCC	GCA	CTA	GCA	TTA	CTC	GGA	ACA
GTA	TTA	ATG	AGC	AAG	GAG	GTT	ACT	\mathbf{ICT}	AAG	GGA	TAT	$_{ m TTT}$	CTT
ATC	AAG	ggg	$_{\mathrm{TTT}}$	CTA	GGA	AGA	TTC	ပ္ပင္ပ	ATG	GAG	AGC	AAG	AGA
GAA	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
TII 1	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	$_{ m LLL}$	GAA	GGA	ACA	GAA
ATG CCA	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GLL	GAA	CLL	TAT	GTT	GAT

2328 GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //

TGA

Figure 17DD

(PCNA) fusion protein PFU DNA POLYMERASE (D141A/E143A/V93R OR E) [Fig.17-DD]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) G, A, or T) D141A/E143A Mutant (GCN is the codon for alanine where N = C, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

540 900 9 TTAIGGGAIG TIICAAGGIC AAGCACAGGG AACCTIGIAG AGIGGIICII ACITAGGAAA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CCACTATTAG AGAAAAAGTT CGAGCCCAAG CACTAGAGGC TGTATATGAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA CATTIACGCT AAGGCATGGA TTCCATTTGC AAAGAGATAC TCTIGCCTIC TATAATGATT TCTTCCATAC TATCAGGGAG ATATTAGCG TTTCGACTTG GGCAACTTAT TGGACAACCT TAACGGGGGA GGGGAAGAAG AGCTAAAGAT AAGGCCCAAT AAAACATAGA TTCTCAGGAT TCGCATTCCC TTAGACCATA GAGATGGAAG AAGATGCAAA CAAGATTAGT GAAGAATACA GTTAAGAAAA GGACATCTTC GAATACGATA AGCAAAGGTG ATTACTTGGA GAGTTTGGAA GAGAGATG ATAAAGAGAT GAAGTCAAGG AGTIGCCAAA TACTCGATGG TCCAATGGAA ATTCAGCTTT GATAGAACTT CAAGATXXXC GGAGACTCAT ACCATTGGAA CCAACATACA GATTAAATTA GATAGAGCAT GATTGAAGAA GGAACATCCC ACCAATGGAG CGAAGGAGAA TACTTATAAT GACGGCTGTA AATAAATCTC GAAAATTTAA GAATTGTTGA AACTTTATT CAGCAGTTGT AAGGCCTAAT CCCTCTATCA ATGAAAATGA TATCAAGCGA AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA ACCTTGAGAG AAGAATTCCT ATGATTCAAA AAGGATCCTG ACATTATAGT CTCATCGACA AGTTATGCAG AAAAGGGCAG TATCATGTAA AGTGGAGAGA GAACTCGGGA AAAGAGAACG CTTCTCAGGG ACCGTGTGGA GCNATAGCNA GTTGAGGTTG ATGCAGAGAA GCAATTTTG AAGATTGTGA AGAGAACATC

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          AGC
                               AGA
                                     GAA
                                          GTT
                                               GAA
                     ATG
                                                                GTT
// ATG
                                                     CHI
                                                          TAT
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Figure 17EE

KOD DNA POLYMERASE - (PCNA) fusion protein [Fig.17-EE]

// Nucleotide sequence (SEQ ID NO: 67) // Nucleotide seguence (SEQ ID NO: 67) Nucleotide sequence (SEO ID NO: 33) Nucleotide sequence (SEQ ID NO: 34)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1080 1200 1260 1320 1380 1620 1140 1440 1020 480 540 720 780 840 960 600 CGGCCACCGC GTCAAGAAGA TAACCGCCGA GAGGCACGGG GGAGAACATA CTACAGCGAC CTGTCATAAG AATTTTCAAG CTTCTACGCC AGCCTGGGAA GGTCACATAC CGGCCAGTCC CCTCAGGAAG GGCCAGAAGA CGTCTCGCCG AGAGGAGAGG AAGGGAGTAC GAGACCAGTT GGACAAGATA CAAGCGCTAC GCTCGCCTTC CCTTATGATA TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CGAGCCGAAG CTTCGATCTC CGTTTATGAA GCTCCTCGAT CGGCTATGCA GLUTAMIC ACID) GTTCAGAAGA AGTTCCTCGG CAGCGATAAG GGCCAGGGTG ATAACTTGGA AGAACGTGGA GGGATGGAAG CTCGCTTAAT TCGAGAGGAA CGGCCTGGGG GATAGAGGAA AAGTACGGCT TTAAGGTAAT TTGAACCCTA AGCTGAAAAT GAGTTCGCCG AGGGGCCAAT TCCTCCGTGT GACGGATACA CGCTTGAGGC AAATAACCAC AAGATGCGAA AGTGGTTCCT GAGGGTTGTG TCACCCACAA CCCCACAGGT GAGACCTCCT ACGGTTACTA TACCCTTCGC TCGACTTCGC GGCCCCGAAC AAGCCCGATG AAAAGGAGCT TACGCTGAGG CAGCACTGGC AACCTCGTTG GAAGGCCACG ATTGACCCGA AACAGCTACT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT GAGTACGACA GGCGACGAGG GAAGTGAAGG TACTCGATGG TCCGATGGAG GCCCAGCTTT GAGCCCGAGA TCAATCATCA ATGCAAGGAA TATGACGTTG ATTIATCCCG AGCCTGCTTG GAGAGCGTAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR CAGGACXXXC GAGGGAGATG ATAAAGCGCT GGCGACAACT GCCCTCGGAA CCCACATACA GATCCTGGCA AATAAACTTC GTTTGCCGTC GATAAACCTG ACGATTCTGC CATTGAGGAA TACTCATCCG TGACATCTAC GCCAATGGAA GGAGAAGGTT AGTCGCCCGC CTATGTAAAA CCTGTACCCC GGAGTGTGCA GGTTGAAAAG TGAGGGCGAG AACCTACAAC AAAAGCTCGG ACAGAGAAGG ACTTCCCAGG GTCAGCCGAA ACCTTGAGAG AGGAGTTCCT TCTCCCGCTC CGGTTAAGCG AACTCTACTT ACGAGGAAGG TGGGCGACAG TAAGACGGAC GGTACTGCAA CCATCAAGGA CAGCAGTTAT AGGGATTAGT CTCTCTACCA TCTCGACGGA ACGLICICAL GGAATGAGCT ATGAAGGAGG ATTTAGATC AGAAGAAGAT GGGCCATCAA ATAACGATGA CTCCTGAAGG GCCTATGAGA GAGGTCTGGA AGCTACGCCG GCCGTCTTCG ACCGGCGAGA CTCTGGGACG CGGCAGAGCT GTGTACCTAG GATACGCTCA TTCTGCAAGG CAGAAGATAA AGGCCCCCT ACGGTTGTAA CTCATAGACA AAAGACCCGG AAGCGCTGTG TATCCTGTGA GAGCTTGGGA TACAGGCAGA CGAGAGCATC GACATTGAAA GTTGACGTCG ATTCAGAGGA

108 162 216 270 324 378 432 486 540 594 648 CCG AAC ATA ACA GCT AAT ACT GCA TTA GAA ATA GGG GTT GCA CIA ATT CTC GAT GAT AGC TAC CIIAAT AGG AAG GAT GGA ACC ACT GAC AAA AAG ggg TGA CAA GAA CTA ATT GAC GGA GCC ATA ACA GAG CTA AAG TAT GTT gcc GAC GAG ACA GIC GAG GGA GAG GAA ACA AAG CAA ATT GAA TIT GAA ATC GTA TIT GAA GGT GCA AAA GAG TIT ATT GAA GCA ATG TLI GAG ATG TTT AAA GTT ATT GAA GTT CII GTT CTG ACA GAG AAA CAA CAA CCA CCA AGA AAA GGA GAA GGA ATA ATA GTC GGT GAA GAA CTT CAG GTT ATG AAA gag gg GCT GII GTT AGA GAG AGC GAG GTT GTA GTT ACC AAG CIG GAG GCC AGT AGA GTT TTA GAC GAA ATC ATG GAT GTA ATG CTA CIA GAA TIC AGT GGA GAA GAT CCA TAT ATC AAC AAG GTG GAG TCC AAT ATA AAG ACA AAA GAA gg GGA GAT GCA CTA GCA TTA TTA AGC AAG CIIATG GAG AAG TAT GTT ACT TCT GGA $_{
m LLL}$ AAG gcc TLICTA AGA AAG AGA GGA ggg AGG AGT ATA GGA ATA CAC AAA CCA GAT ATA GAT GIC AGC ATG CCA GAC ACC GCA ATG AAG ACA CTT AAA $_{
m LLL}$ ACA GAA GAA GGA AGC TCA CIC GII ATG AGA GAA GAA CTT TAT

Figure 17FF

(PCNA) - KOD DNA POLYMERASE fusion protein [Fig.17-FF]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 34) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
. .	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
A GAC	ලලල	CTC	GTT	TTA	GCA	CIC	GAT	GAA	CTA	AGC	GAT	ATT	
r ATA	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ပ္သပ္သ	TAC	:
A CTT	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ပ္သပ္သ	ATA	ACA	AAG	TAT	GAG
CAA	ACA	GAC	ACA	AAG	CAA	GAA	GTC		GAG	GAG	GGA	GAG	GAA
r GCC	GTT	ATT	GAA	GCA	ATT	ATG	_	-	GIT	GAG	CIT	ATG	GTT
3 TTT	AAA	CTG	CCA	AAA	ACA	_	GGA	-	GAA	CAA	GGA	CAA	AGA
A GAG	TTT	GTC	GAA	GGT	ATA	GAA	CIT	ATA	CAG	GTT	AAA	ATG	CCA
A AAA	gcg	GTT	GTT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	CCC	GCT
r GCA	gcc	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
V GGT	GAG	AGT	GAA	CTA	TTC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
r gaa	GAT	CCA	TAT	ATC	AAC	CIA	AAG	GTG	GAG	TTG	TCC	AAT	TIC
\ TTT	ATA	GAT	AAA	AAG	GAA	င္ပင္ပ	GCA	CTA	GCA	TTA	CIC	GGA	ACA
GTA	TTA	ATG	AGC	AAG	GAG	GTT	ACT	\mathtt{TCT}	AAG	GGA	TAT	TTT	CTT
A ATC	AAG	gcc	$_{ m LLL}$	CTA	GGA	AGA	TIC	ggg	ATG	GAG	AGC	AAG	AGA
GAA	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
TTT \	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TTT	GAA	GGA	ACA	GAA
ATG CCA	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GTT	GAA	CLT	TAT	GLL	GAT

70048700487

//ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60 480 ACGATICIGC CATIGAGGAA GICAAGAAGA TAACCGCCGA GAGGCACGGG 180 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120 CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT GGACAAGATA GCICGCCIIC CCTTATGATA TCTCCCCTAC TGTGAAGGAG CTATCTGAAA CAAGCGCTAC AGCTGAAAAT GAGGTCTGGA AACTCTACTT TACTCATCCG CAGGACXXXC CAGCGATAAG TGACATCTAC GAGTACGACA TACCCTTCGC TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT AGAACGTGGA TCGACTTCGC TCCTCCGTGT GCCAATGGAA GGCGACGAGG GGCCAGGGTG ATAACTTGGA GAGGGAGATG ATAAAGCGCT ACGITCICAL AACCIACAAC GGGGACAACI CAGCAGTTAT TCTCGACGGA CTCTCTACCA ACGAGGAAGG AGGGATTAGT GTTGACGTCG AAAGACCCGG CTCCTGAAGG ACGGTTGTAA CGAGAGCATC AGCTACGCCG CTCATAGACA GACATTGAAA

Figure 17GG

(PCNA) -Vent DNA POLYMERASE FUSION PROTEIN [Fig.17-GG]

// Nucleotide sequence (SEO ID NO: 35) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 67) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

108 216 324 378 432 486 540 648 162 594 CCG AAC ATA ACA CCA GCT AAT ACT GCA ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA GAA ATG CCA TIT GAA ATC GTA ITT GAA GGT GCA AAA GAG TIT GCC CAA CIT ATA GAC CIC GTT TTA CIC GAA GAT ATT GCA CTA AGC GAT TAC CTA AAT AAG GCC ACA ATT GGA GIT GAC ACA AAG GAC ACC GGA ACT CTA AAA GCC AGG ATA AAG TAT GAC AAG GAG GAG GGA GAG GAA ATT CAA GAA GIC CCA AGT AGA GTT GTC CTG ATT GAA CCA GAA GGT AAA GCA TTT GII GAG ATG GTT GAG ATG GGA GAA ATA ACA ATT GGA CTT CAA GA CCA AGA ATA AAA GAA ATG GAA AAA GLL CHI CAG GTT GAG GLL CCC GCT CTA AAG AGA GTA GIT AGC ACC GAG TTA GAT GAC CTG GAA ATG TAT GAA GTT GTA GAC ATC GAC ATG TIC GAA AGT ATA GTT GGA ATC AAC GTG $_{
m TTG}$ TCC AAT TTC CTA AAG GAG AGG GCC ATG GAT CIC GGA ACA TIT AGC AAA AAG TTA GAA GCA GCA CCC CTA AAG TAT GAG TTT CTTGTT AAG GGA ACT TCT CIA AGC TIC GGA GAG AGA ggg ATG ATA AAG ATA GIC ATA CAC AAA ${
m LLL}$ GAT CCA GAT AGC ATG TCA AGC GAC $_{
m TTT}$ GTT ACA CTC AAG CHI GTT AAA TAT GGA GAA AGA ACA CTT GAA GAA GAA GAT ATG

540 9 300 360 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT GAGACATGGA AAGGGAAGTT GGGCAAAATA CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT AAAGACCCCG AIGIGAIAAI AACIIACAAI GGGGACAAII TIGAITIGCC GIAICICAIA TGTTAAAGAA GAATATGACA TACCCTTTGC TATTGAGGAG ATAAAGGCAA TAAAGGGCGA GTCAGGAAAA AATTTTGGG CAGCTATGCG TTGTTCAAGT TCCCATGGAG GGAGACGAGG AGCTTAAGCT GAATTIGGAA AGGGCGAGAT AAAATATCGA CAAGACXXXC ATCACATGGA ATAAAGCGTT TGACATTTAC GGCCAGAGTA TGCAGTGAAA CGAGCATCCC AAGAGAAATG TGAGGGAGAT GGGAGTTTAA CAGCTGTGGT AGCTCATTTT AGGGCTTGAT CGTTTTATCA ATGAAGAAGA TGTCCAATGA ATGACTCCGC GAGTGCTCGA CTTCTCAAAG AAAACTGTGA AGGGAACATC CTCATAGACA AAAGAGAACG GAAGTCTGGA GATATTGAAA AGTTATGCCG GTCGATGTTG

Figure 17HH

Vent DNA POLYMERASE - (PCNA) FUSION PROTEIN [Fig.17-HH]

Nucleotide sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 35) // Nucleotide sequence (SEQ ID NO: 67)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

1140 1500 1020 1080 1200 1260 1320 1440 1380 900 780 900 960 540 9 840 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG GCTGATAGGT AGGTTTGTGG TACTCACAAC TCCGATAGTA GAGACATGGA AAGGGAAGTT GGGCAAAATA CAAGCGTTAT AATAATGATT GTATCTTTA AGAGTATAAA GGACTTAATT TATATATGCT CCTTGCCTTT ACATCCCGAA TGCCGCTATA TGCTAGGGCA CGCATGGGGG TGTTAAAGAA GTATCTCATA AATCCACTTT CGGCTATATG TAAGGTTCTT TTTGCCGTAT TGAGGCAGTT CGAAAAGAAA AATTTTGGG AGGGCGAGAT TCAAGGGTAG TTCAGCCCTA AGCTTAAGCT AAAATATCGA TTGTTCAAGT GGGACAAAGA CGTATACGCT CAGAGGAAAT CAATGGAAGA AGCTGGCAAA TCGTGGAGTG CTGATGAGGA AGCCAGAAAA CAATAATAGT ACGATGTTGC TTGACCCGAT ACAGCTATTA AAAGCGTTAC GATAAGAGAA ATAGAGGAAA AGTTCGGCTT TAAAGGGCGA CAGCTATGCG TACCCTTTGC TTGATTTGCC CCATACTCGG GTCAGGAAAA GGAGACGAGG ATCACATGGA ATGGAAGCTG ATAAAGGCAA GAATTTGGAA GGGGACAATT ACCGGCAACC TATGTAAAAG TGTAAGAATT TTGCTTGCAA GAATGTGCTG GAATATGACA ATAAAGCGTT GTCTTAGGAA GCTGTGGAAA AACCTCCCAA AAATTAGGAG GCCCAGTACT CCGAACAAAC AAATCCACAA GACCCTCATT CTGTACCCTT CAAGACXXXC TTTATTCCCT GGCCAGAGTA AAGGACGATA GAGATCAAGC TATTGAGGAG AGTTCGGCTT ATTCTTCCCC AAAAGAGGGC CTTTCCGGGC GTACTCGAAG AATAGAACTT TGCAGTGAAA CGAGCATCCC TCCCATGGAG TGAGGGAGAT AAGAGAAATG AACTTACAAT TGATAGTTTT AACCAAAAGC GAAAAACTA CCTGGGAGGA TTTCCGCAGT GAAGAAAATG GGCTATTAAA TGACATTTAC TGAACTTGCA TAGAGATGAC ATGACTCCGC GAGTGCTCGA AAAAGCTGGG CAGTTGTGCG AAGAAAGCAT TCGGGAAGGA ATACCCTTGA AGGGCTTGAT ATGAAGAAGA TGTCCAATGA ATGTGATAAT AGAGGATGGG TTTTAGGAAA ACGCGAGGAA GAACAACTTA TTTATTTGGA TCTGCAAGGA AAGATATAAA AGGCAAGATG GGGAGTTTAA CGTTTTATCA GGGACGTCTC ATAGGCAAAG AGCTCATTTT CAGCTGTGGT CTTCTCAAAG AGACACTACA AAACGGGCAG GTATCCCCAG GAAGTCTGGA AGTTATGCCG TATGAAGCAG ACGTATGAGC GCAATGAGGC SGGTATCCTA AAAGAGAACG AAAACTGTGA AGGGAACATC CTCATAGACA GTCGATGTTG AAAGACCCCG CCCAAGATTC **IGGGAAACAG** CAAAGTGTAT AGGGTGGCAT CGGCGCTTAA GAAAATATCA GGATATAGGT ATGCTCGATT GATATTGAAA GATCTTTCC

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CTGACGGCTT TTATGCCACA ATACCCGGGG AAAAGCCTGA ACTCATTAAA
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                 AAGAAAGCCA AGGAATTCCT AAACTACATA AACTCCAAAC TTCCAGGTCT
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                                       GCTTTTACTT GAGGGATTC TTTGTTACAA AAAAGCGCTA
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     ACC GCA AGT AAG TTA ATA GAT GAG GCC GCG TTT AAA GTT ACA GAA GAT GGG ATA
             CCG
ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC
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                                      GTT
                                                   TCT
                                                                GGA
                          CIA
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                                 AAA
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             AGC ATG
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                         GAC
                                                                                    GAA
                   TCA AGC
                                 AAG
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                                             CTT
                                                    AAA
                                                          TTT
                                                                 GAA
                                                                       GGA
                                      AGA
                         ATG
                                 CTC
                                            GAA
                                                          GAA
                                                                CTT
                                                                       TAT
                                                                             GLT
                                                                                   GAT
                                                   GIT
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Figure 1711

Deep Vent- (PCNA) DNA polymerase fusion protein [Fig.17-II]

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 180 300 360 480 540 900 9 780 840 900 960 1080 1140 1200 1260 1500 240 420 720 1020 1320 1380 1440 CGATTATAAG GATTTTCAAG TTAGACCTTA CATTTACGCT ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC GATAAGGGAG TGAGCCAAAG GGCCTGGGAG GGTAACGTAC CGGCCAGCCC CCTCAGGAAG CGAGAGAAGG CTGGGAGGGG TAACGICICA AGGGTGTAGG GAATACGATG TCGCCCCAGA GGTTGGGCAC ATTGGATGAA GAAGATGCTT CAAAATCCTG GCAAACAGCT ATTATGGGTA TTATGGGTAC AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT GGATAAGATA GAAGAGGTAC GCTCGCATTT TATAATGATA AGTTTATGAG CTATCTAGTT CTTTGACCTC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CCCAGCCTGC TCAAGAGGTT CCGCAATAAG GAGTICGCGA AGGGGCCCAT TCCTCAAGGT GGGACGGTAG GAAGGATACA CCAACATACA CCCTCGAGGC TACGCTCACG AGATAGCTGA AGGATGCAAA CCCAATGGAG GCCCAGCTTT CAAGGTTAGT TTCAACTGGC AACTTGGTGG AGTGGTACCT GGCTCCAAAC AAGCCGGATG AGAGGGAGTA TAATCACCCA CAATCGAGAA TTCCGTTCGC GGCGATGAAG AGCTCAAGTT AGAAAGGGCT TCGACCTTCC AGTIGCAAAG TATICAAIGG GGGATACGTT AAGGAGCCGG AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT GACAGCGGTG GAGATAAAGG GATGAAAGCT TCTAAAGACC ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC GAGTACGACA GAGGGAGATG ATAAAGCGGT GGCGATTCTT AAAAGCTCGG GATAAAGCTA CCCCTGGGAA CCCTCGATAA CAGGACXXXC GGGGTTTATC TTAGGAGAAC GATAAACCTC GGAGAAAGTT GAGCCTGTAC TGACATCTTT TCCAATGGAA CGAAGGGGAG GGCTGTACTT TGAACACCCT TACCTACAAC AGGCAAGAAA TAAAAAGGAA TTTCTAGGTC AAGGCCTAAT GGGAGTTCTT GCTACGCTGG GATTACAGGC AACGGGCAAT ATGAGGAAGA TTGGGGATAT GAAAGCCAAA GACTGGAGAG GCCTACGAGA GGAATGAATT TAGATTTCAG TGAACAGGGA AGGACTTCCC CCGCAGTTAT TTTCCAGCGA ATGTTATAAT CCCTCTATCA CTCCTCAAAG CTAAGGGAGA CCGGATACGC AGAGAGCATT AGCTATGCTG AAAGATCCCG ATGCAGAGGC TACCACGTGA CTGTGGGATG AAGTTCTGCA GAGGTATGGA CTAATAGACA GACATAGAAA GTCGAGGTAG AAGAGGGCCG GCAATCTTCG ACTGGAAAGG GAGCTCGGTA TTAGTTTCCC

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1920
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           1620
                                       1740
                                                                                                            2040
                          1680
                                                      1800
                                                                    1860
                                                                                                                          2100
                                                                                                                                       2160
                                                                                                                                                                                  2328
                                                                                             TCCAGAAAAG
                                                                                                            AGGTCCGCAC
                                                                                                                                                                   GTGGCAGAAG
GGGGAGGGAA
            CTTATACATA
                                                      GATAGATGAG
                                                                    CGAAATAGCC
                                                                                  TGAGGAGGCA
                                                                                                                          CATGGTGATA
                                                                                                                                        TGCAGAGGAG
                                                                                                                                                      GGTTTTACCT
                          AAAGAAGAAA
                                         GCTTGAGTAC
                         CCGAGGAGAT
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TTACGGCCTG
             GGTTCAAAGT
                                                                                 CCTAGAGGCT ATCCTAAAGC ATGGCAACGT
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                                                                                                            ACAAGGCTAT
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GTIGGTACTG TAAGGAGTGC GCAGAGAGCG
             GGAACTGGAG GAAAAGTTCG
                          GGGCCAAAAC
                                       AAGCTCCCAG
                                                     GTTCTTCGTG
                                                                    GGGCCTTGAA
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                                                                                                                          AGCCGCTAGA
                                                                                                                                                                   GGCCTTTGGG
                          CACAATICCI
                                         TATAAACGCC
                                                                                                                                                       GTATGACGCT
                                                                                                             CACGAGGCCC
             TCGTAAGGAA
                         GACTCTACGC
                                                     ACGTGAGAGG
                                                                   TAATCACTAG
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                                                                                              TTAAGGAGGT
                                                                                                                                        TGCTGAGGGG
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                                                                                                                                                                                  CAGGTCTTAC
                                         TCGTAGATTA
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            TATATAGAGT
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SCAAAAGCCC
                                                     GAGGGCTTCT
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                          GACACAGATG
                                        GCCCTAGAGT
                                                                    GAAGGGAAGA
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486
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     929
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GTA
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     ACC
               TCA
                    ATG
                              AGA
                                   GAA
                                              GAA
                                                   CIT
// ATG
                                         GTT
                                                        TAT
```

Figure 17.J.J

(PCNA) - Deep Vent DNA polymerase fusion protein [Fig.17-JJ]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

54	108	162	216	270	324	378	432	486	540	594	648	702	
GAC	ATA	CCG	AAC	ATA	ACA	CCA	GCT	AAT	ACT	GCA	GAA	AGA	
ATA G	ggg	CTC	GTT	TTA	GCA	CTC	GAT	GAA	CTA	AGC	GAT	ATT	
CTT A1	GAT	AAT	GGA	ACC	ACT	GAC	AAA	AGG	AAG	AAG	ပ္သင္ပ	TAC	:
CAA CI	GAA	CTA	ATT	GAC	GGA	GTT	CTA	ပ္ပပ္ပ	ATA	ACA	AAG	TAT	GAG
GCC CA	ACA	GAC	ACA	AAG	CAA	GAA	GIC	ATT	GAG	GAG	GGA	GAG	GAA
-	GTT	ATT	GAA	GCA	ATT	ATG	GAA	TIT	GTT	GAG	CTT	ATG	GTT
G TTT	AAA	CTG	CCA				GGA				GGA	CAA	AGA
A GAG	TTT	GIC	GAA	GGT	ATA	GAA	CII	ATA	CAG	GTT	AAA	ATG	CCA
A AAA	gcg	GTT	GLT	AGA	GAG	GTA	GTT	AGC	ACC	GAG	GTT	င္ပင္ပ	GCT
T GCA	ggg	AGA	GTT	AAG	TTA	GAT	GTA	GAC	GAA	ATC	ATG	ATG	CTG
A GGT	GAG	AGT	GAA	CTA	TIC	ATA	GTT	AGT	GGA	GAC	GAC	GAA	CTA
T GAA	GAT	CCA	TAT	ATC	AAC	CTA	AAG	GIG	GAG	TIG	JCC	AAT	TIC
GTA TTT	ATA	GAT	AAA	AAG	GAA	CC	GCA	CIA	GCA	TTA	CIC	GGA	ACA
ATC GT	TTA	ATG	AGC	AAG	GAG	GTT	ACT	TCT	AAG	GGA	TAT	TTT	CTT
	AAG	gcc	$_{ m TTT}$	CTA	GGA	AGA	TTC	ဗ္ဗင္ဗ	ATG	GAG	AGC	AAG	AGA
T GAA	AGT	AGG	ATA	CAC	AAA	TTT	CCA	GAT	ATA	GAT	GTC	ATA	GGA
A TTT	GCA	ATG	AGC	GAC	AAG	ACA	CTT	AAA	TTT	GAA	GGA	ACA	GAA
ATG CCA	ACC	AGC	TCA	ATG	CIC	AGA	GAA	GTT	GAA	CTT	TAT	GTT	GAT

//ATGATACT	rg ACGCTGACT	TA CATCACCGA	G GATGGGAAG	C CGATTATA	//ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG	9
AAAGAAAACG	GCGAGTTTAA	AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT	GACAGAAACT	TTAGACCTTA	CATTTACGCT	120
CTCCTCAAAG	ATGACTCGCA	CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG	GTTAGGAAGA	TAACCGCCGA	GAGGCATGGG	180
AAGATAGTGA	GAATTATAGA	AAGATAGTGA GAATTATAGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG GAGGCCGATT	GTAAGGAAGA	AGTTCCTGGG	GAGGCCGATT	240
GAGGTATGGA	GGCTGTACTT	GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA	CAGGACXXXC	CCGCAATAAG	GGATAAGATA	300
AGAGAGCATT	CCGCAGTTAT	AGAGAGCATT CCGCAGTTAT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC	GAGTACGACA	TTCCGTTCGC	GAAGAGGTAC	360
CTAATAGACA	AAGGCCTAAT	CTAATAGACA AAGGCCTAAT TCCAATGGAA GGCGATGAAG AGCTCAAGTT GCTCGCATTT	GGCGATGAAG	AGCTCAAGTT	GCTCGCATTT	420
GACATAGAAA	CCCTCTATCA	GACATAGAAA CCCTCTATCA CGAAGGGGAG GAGTTCGCGA AGGGGCCCAT TATAATGATA	GAGTTCGCGA	AGGGGCCCAT	TATAATGATA	480
AGCTATGCTG	ATGAGGAAGA	AGCTATGCTG ATGAGGAAGA AGCCAAAGTC ATAACGTGGA AAAAGATCGA TCTCCCGTAC	ATAACGTGGA	AAAAGATCGA	TCTCCCGTAC	540
GTCGAGGTAG	TTTCCAGCGA	GTCGAGGTAG TTTCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG	ATAAAGCGGT	TCCTCAAGGT	GATAAGGGAG	009

TT 660	72			AG 900		CC 1020	AG 1080	GG 1140	GG 1200	CA 1260	AC 1320	AA 1380	TT 1440		156	TA 1620	AA 1680		180	186	192	198	AC 2040		AG 2160		AG 2280	2328
CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	TAACGICICA	GGTTGGGCAC	ATTGGATGAA	GAAGATGCTT	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA	GCTTGAGTAC	GATAGATGAG	CGAAATAGCC	TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAAG	
TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	AGATAGCTGA	AGGATGCAAA	CAAGGTTAGT	AGTGGTACCT	AGAGGGAGTA	AGAAAGGGCT	TAATCACCCA	TCGCCCCAGA	TCAAGAGGTT	CAATCGAGAA	ATTATGGGTA	TTACGGCCTG	GGTTCAAAGT	CCGAGGAGAT	GGCTGTTGGA	AGTATGCGTT	GGGACTGGAG	ATGGCAACGT	ACGAAATACC	ACAAGGCTAT	TGAGGCCTGG	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	AGAAG TAA
GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGGCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GTTCTTCGTG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
ATGTTATAAT	AAAAGCTCGG	TTGGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC
AAAGATCCCG	AAGAGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGCCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

Figure 17KK

JDF-3 - (PCNA) fusion protein [Fig.17-KK]

Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 67) Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 67)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCCTCGG CAGGTCTGTGGAGGTCTTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGGTCATCGACATCTACGAGTACGACATACCC TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAAGAAGTTTAAACTCATGTCCTTQGAQATQGAGACGCTCTACCACGAGGGAGAAGAGTTTGGAA A CUTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTTCGGCAAGCCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGCTTGAGAG acgecegregetaceaceaagecegagegegegacateregaacaatategretatactagactrtegagectetetadecaficaateataateaceacaacaacatece CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGGGGACGCTGAAAACAGTCAAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCC actegageegagatagegaagagaegegaggegaggetittiggaggegatacteaggeacgtigaagagagegegeteagaattgteagggaagteacegaaaagetgageaa **ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTTCGACCTTTATCCAGTCATAAGGCGCACCATAA** GGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGCTTGAGGAAAAGTTCGGTTTTAAAGTCCT GTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGTTCGACCACGACGACGAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCG GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGA TGATCCTTGACGTTGATTACATCACCGGAGAATGGAAAGCCCGTCATCAGGTCTTCAAGAAGGAGAAGGCGAGTTCAGGATTCAGGATTGAATACGAGTTCGAGCCTACTTCT GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

ATG CCA TTT GAA ATC GTA TTT GAA GGT GCA AAA GAG TTT GCC CAA CTT ATA GAC

54

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         AGC
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                   GAG
                        GTT
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                                                GTC AGC
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                             CCA
                                 GAT
                                      ATA
                                           GAT
                                                          GGA
              CAC
                   AAA
ACC GCA
AGC ATG
                            GAA CTT
GTT AAA
                                                     GTT ACA
         TCA AGC
ATG GAC
                                                TAT GGA
                                                          GAT GAA
                   CTC AAG
                        AGA ACA
                                      GAA TTT
                                           CTT GAA
```

Figure 17LL

(PCNA) - JDF-3 fusion protein [Fig.17-LL]

Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 67) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

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108
162
216
216
270
324
432
432
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Figure 17MM

Sac7d gene (ACCESSION No: M87569) [Fig.17-MM]

Nucleotide sequence (SEQ ID NO: 69) Amino acid sequence (SEQ ID NO: 70)

36 108 54 162 67 201 D GAC s TCA N G K T G R G A V S E K D A P K E L AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA M V K V K F K Y K G E E K E V D T ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAA GAA GTA GAC ACT F T Y D TTT ACC TAT GAC K I K K V W R V G K M V S AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC L D M L A R A E R E K K * TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG TAA

igure 17NN

Sac7d-Taq DNA polymerase fusion protein [Fig.17-NN]

Amino acid sequence (SEQ ID NO: 70) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 65)

DGAC M V K V K F K Y K G E E K E V D T S ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA L TTA K I K K V W R V G K M V S F T Y D AAG ATA AAG ATT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC N G K T G R G A V S E K D A P K E AAT GGT AAG GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA

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Q A [X]V Y G F A K S L L K CAG GCG [0] GTC TAC GGC TTC GCC AAG AGC CTC CTC AAG
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Figure 1700

Taq DNA polymerase-Sac7d fusion protein [Fig.17-00]

Amino acid sequence (SEQ ID NO: 66) /Amino acid sequence (SEQ ID NO: 70) Nucleotide sequence (SEQ ID NO: 65) //Nucleotide sequence (SEQ ID NO: 69)

9 9 9 // GGC GGC GGT

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Q A [X]\underline{\mathrm{M}} Y G F A K S L L K CAG GCG [0]\underline{\mathrm{G}}TC TAC GCC TTC GCC AAG AGC CTC CTC AAG
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Figure 17PP

Pfu DNA Polymerase (WT) -Sac7d fusion protein [Fig.17-PP]

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ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc
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Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 69)
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aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgetecaa geagageege tecaatggat aacaceeetg tteeegeace caagteeget acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa gtagaagcgg cactactcag atgettecee aggaatgagg ttgttgtage tenteeenga aagattgaga tgttcttgg //

^{//} ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA

TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //TGA

Figure 1700

Sac7d - Pfu DNA Polymerase (WT) fusion protein [Fig.17-QQ]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 61)

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ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc cccagtcgc
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Figure 17RR

Sac7d - PFU DNA POLYMERASE (V93 R OR E) fusion protein [Fig.17-RR]

Nucleotide_sequence (SEQ ID_NO: 69) // Nucleotide sequence (SEQ ID_NO: 27) Nucleotide sequence (SEQ ID NO: 69) //Nucleotide sequence (SEQ ID NO: 28) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGC, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GAC GAC GAA TTA GTA GAC ACT GCT CCA AAA TTT ACC TAT GAA TCC GAT AAA GAG AGA GGA GCT GTA AGC GAG AAA TGG AGA GTA GGC AAA ATG GTG GAA GGT AAG AAG TAT TIC GGT GCA AAG AAG ATA AAG AAG GTT GTA ACA TTA AAG GGT AAG ATG GTG TTA GAC ATG AAT

1320 1380 1560 1200 1260 1440 1500 1620 1680 1740 1800 1020 1080 1140 //ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 540 600 999 720 840 900 960 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 AAGGCATGGA 180 GGCAACTTAT TCAAAGAAGG CAATGTTTCT AATACTCCTT TTATGGCTAT AAAGAAAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA TGAAGAAGCT ACCAGAGAAG CAAGCCTATT AGAAAAGTT AAAGAGATAC AGCCTGGGAA GTGGGAAAAC AGTAGGCCAC GTTAGAGGAA GGGAAGAAAG TATAATGATT CGAGCCCAAG TGGACAACCT ACTTAGGAAA CCTCTACATT TCTTCCATAC TATCAGGGAG ATATTTAGCG TTTCGACTTG TGTATATGAA TCTTGCCTTC CTICICAGGG AIGATICAAA GAITGAAGAA GITAAGAAAA TAACGGGGGA GGAACATCCC CAAGATXXXC CCACTATTAG GGACATCTTC GAATACGATA TTCCATTTGC ATGAAATTCC TTCTCAGGAT AGATAGCAAA AAGAGGAGTA TAATTACCCA GGTATGCAGT GTTGAGAAAA AGTTTCTCGG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT GAGTTTGGAA AAGGCCCAAT AAAACATAGA TCGCATTCCC GAGATGGAAG GAAGAATACA CACTAGAGGC AAGATGCAAA CAAGATTAGT AGTGGTTCTT AAAGAGCCAG AAAAGGGGTT TCGCTCCTCA TGGGACATTT CTATAGAAAA TCTACGGATA TTACTGCCTG GATTTAAAGT GTGAGGAAAT GAGATTGGAG ACGGAGATGT GACTGCTAGA AGA GCA GAA AGA GAG AAG AAA // ATTACTTGGA ATAAAGAGAT GGAGACTCAT ACCATTGGAA TACGCCGACG TACTCGATGG AACCTTGTAG AAGCCAAGTG CCCTCGATTA AACTATGATA CCAAGTCTCT TGGTTTAGAG ATAGTTAGGA ATACTAAAAC CTTGCCAATT TCCAATGGAA ATTCAGCTTT GCTGAGAGCG AAGCTCCCTG ACGAAGAAGA GAAGTCAAGG CCAACATACA ACTCAAGATC GCAAATTCTT GGAGGAGAAA GAAAAGTTTG GATTAAATTA AGTTGCCAAA AGCTCCAAAC TGGATTCGTT GGGATGCAAG ATTCTTCGTT TTTGGAGACA TGTAGAGAAG CGAAGGAGAA AGCAAAGGTG GAGAGAGATG AAGCACAGGG AGCCCTATAT TGGTTTTATA AATGAAGGAA AAAACTCTTA CATAAATTCA AATACAAAAG TACTTATAAT GACGGCTGTA AATAAATCTC GGAGAAGGTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA CAGCAGTTGT GCTACACAGG AAAAAGCGAT TAAAAGAAGT GAATTGTTGA AACTTTATTT AAGGCCTAAT CCCTCTATCA ATGAAAATGA ACATTATAGT AAAAACTTGG GAAAGCCAAA ACCTTGAGAG TTTCAAGGTC TAGATTTTAG GATGGTACTG ATAAGAGGGG TATCAAGCGA TAGGCGATAT TAACAAGGAC AAGAATTCCT GAAACGAAGT TAAATCTTGA AGGACATCCC TTAAGACAAA TAGTATGGAA GTCTCTATGC TCATTACTCG AAGCTAGAGT TTGTAAAATA ACCGTGTGGA AAAAGGGCAG GACTATAGAC GCTCTAGAAT GAAGGGTTTT AAAGAAACTC GTGAGAATAG AGAGAACATC CTCATCGACA AGTTATGCAG AAGGATCCTG ATGCAGAGAA AGTGGAGAGA GAACTCGGGA ATAGTATACC AGACAAAAGA GAAGGAAAAG GATATAGAAA GTTGAGGTTG TATCATGTAA TTATGGGATG CTCAGGGAGA AAGTTCTGCA TACATCGAGT AAGATTGTGA GCAATTTTG GCCTACGAAA CCCGATACTC GCAAAAGCAA GACACTGATG

2100 2160 2220 2280 2328 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT GGTTCTTCCA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG AGCTGAGGAA CGATGGTCCA ATTAGCAATA GGGCAATTCT TGGAGAACCA ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC // GAATATTACA GTATGACGCA TACTTAGAGG AAAAGCACAA GGATATTGGA TACGATCCCA GTAGCTGTTG GGATACATAG GCGGTACTTA // TGA

Figure 17SS

PFU DNA POLYMERASE (V93 R OR E) - Sac7d fusion protein [Fig.17-SS]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 69)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1020 480 420 540 99 900 ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT CATTTACGCT TTTCGACTTG TGTATATGAA CTGTTATTAG GCTATTCAAA CCACTATTAG AGAAAAGTT AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG ATATTTAGCG CGAGCCCAAG AGCCTGGGAA GGCAACTTAT GLUTAMIC ACID) TTCCATTTGC AGCTAAAGAT AAAACATAGA GAAGAATACA CACTAGAGGC GGAGAAGGTA TACGCCGACG AGATAGCAAA TTAGACCATA TTCTCAGGAT TCGCATTCCC GAGATGGAAG AGTIGCCAAA TACTCGAIGG AAGAIGCAAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GAATACGATA GGGGAAGAAG GGAGACTCAT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC AGCAAAGGTG ATTACTTGGA GAGAGATG ATAAAGAGAT GACGGCTGTA GAAGTCAAGG CCAACATACA GATAGAACTT CAAGATXXXC ACCATTGGAA GAAAATTTAA GATAGAGCAT TACTTATAAT GGAACATCCC GGACATCTTC AATAAATCTC ACCAATGGAG GATTAAATTA GAACTCGGGA AAGAATTCCT CAGCAGTTGT ACCTTGAGAG ACCGIGIGGA AACITIAITI AAGGCCTAAT CCCTCTATCA ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA AAAGAGAACG CTTCTCAGGG ATGCAGAGAA TATCATGTAA AAGATTGTGA AGAGAACATC CTCATCGACA AGTTATGCAG AAGGATCCTG AAAAGGGCAG AGTGGAGAGA GATATAGAAA GTTGAGGTTG GCAATTTTG

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                                                   ATAGTATACC
                                                                                     AAGTTCTGCA
                                                                                                                                                            TACATCGAGT
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Figure 17T7

PFU DNA POLYMERASE (G387P/v93R OR E)-Sac7d fusion protein [Fig.17-TT]

Nucleotide sequence (SEQ ID NO; 29) // Nucleotide sequence (SEQ ID NO; 69) Nucleotide sequence (SEQ ID NO: 30) // Nucleotide sequence (SEQ ID NO: 69)

2280 2160 2220 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG GGATATTGGA ACAAGACAAG GTAGCTGTTG GCGGTACTTA

GAC TIA GTA GAC ACT ACC TAT GAC CCA AAA GAA 2328 GCT $_{
m LLL}$ GAA TGA GAG AAA GTG TCC GAG AAA GAT GCA GAA AGA GAG AAG AAA // TICCIGGCII AACAITAAAA AAICC // gaa atg TAT AAG GGT GTA GGC AAA GCT GTA AGC GGA AAG AGA ATG TTA GCA AGA TTC AAG ACA GGT AGA GTA AAG AAG AAG AAG AAG AAG GTT AAG TCGGCCTAAC AAG AAG TTA GAC GTG AAT GGT AAG ATA // ATG

Figure 17UU

PFU DNA POLYMERASE (G387P/V93R OR E) -Sac7d fusion protein [Fig.17-UU]

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 69)

// Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEO ID NO: 30)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 300 240 or T) TTAGACCATA CATTTACGCT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT AAAGAGATAC CTGTTATTAG GCTATTCAAA AGAAAAAGTT CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAAGAT TCTTGCCTTC G387P Mutant (CCN is the codon for Proline where N = C, G, A, V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CCACTATTAG CAGCAGTIGT GGACATCTIC GAATACGATA TICCATITGC ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CAAGATXXXC GGAACATCCC AACTTTATTT ACCGTGTGGA AGAGAACATC

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GAC GAC GAA GAC ACT TAT CCA AAA ACC GIA GAA $_{
m LLL}$ GCT TGA AAA TCC GAT GAA GAG GTA GGC AAA ATG GTG GAG AAA AAG AAA GTA AGC GAA AGA GAG TAT AAG GGT GCT AAG AGA GGA GCA TIC TGG AGA AGA GCA AAG GTT GGT GTA ACA AAG AAG AAG AAG ATG AAG ATA GGT GAC GIG AAT // ATG

Figure 17VV

SAC7D-PFU DNA POLYMERASE (D141A/E143A/V93R OR E) fusion protein [Fig.17-

Nucleotide sequence (SEO ID NO: 69) // Nucleotide sequence (SEQ ID NO: 32) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 31)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

//ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60 540 900 840 900 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120 9 GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT TATCAGGGAG TGTATATGAA AGCCTGGGAA GGCAACTTAT AGAAAAAGTT ATTACTTGGA AAAACATAGA TCTTCCATAC ATATTAGCG TTTCGACTTG ACTTAGGAAA AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG CAGCAGTIGI GGACATCITC GAATACGATA ITCCATITIGC AAAGAGATAC TATAATGATT CGAGCCCAAG TCTTGCCTTC TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG AACTTTATTT GGAACATCCC CAAGATXXXC CCACTATTAG GAGAGAGATG ATAAAGAGAT TTCTCAGGAT CACTAGAGGC TACTTATAAT GGAGACTCAT TCGCATTCCC ACCAATGGAG GGGGAAGAAG AGCTAAAGAT CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT GAGATGGAAG GAAGAATACA AGATAGCAAA TACTCGATGG AAGATGCAAA CAAGATTAGT AGTGGTTCTT GAAGTCAAGG TACGCCGACG AACCTTGTAG ATTCAGCTTT GATTAAATTA ACCATTGGAA CCAACATACA TCCAATGGAA AGCAAAGGTG AGTTGCCAAA AAGCACAGGG GACGGCTGTA AATAAATCTC GGAGAAGGTA GCCTACGAAA GAAACGAAGT GAATTGTTGA AAGGCCTAAT ACATTATAGT TAACAAGGAC ACCTTGAGAG AAGAATTCCT TTTCAAGGTC CTTCTCAGGG ATGATTCAAA ATGAAAATGA TAGGCGATAT CCCTCTATCA AAAAACTTGG TATCAAGCGA GAAAGCCAAA AGAGAACATC CTCATCGACA AGTGGAGAGA GAACTCGGGA AAGGATCCTG TTATGGGATG ACCGTGTGGA GCNATAGCNA AGTTATGCAG GTTGAGGTTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTG AAGATTGTGA

1200 GCTACACA [CC N] GTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1440 1500 1740 1800 1860 1920 1980 2040 2160 2280 TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 1560 1680 2100 2220 GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC AGGTCCTCAC GTTAGAGGAA TTATGGCTAT GGGAAGAAAG GCTTGAATAT AATAGATGAA TGAAATTGCA ACCAGAGAAG AATACTCCTT CCTCTACATT AAAGAAAAAG TGAAGAAGCT AATGGTAATT AGCTGAGGAA GGTTCTTCCA ATACCAAAAG TCTACGGATA GACTGCTAGA GGTATGCAGT TAAAGCCAGG AAGACCTCAG CTATAGAAAA TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GATTTAAAGT TGGTTTAGAG ATAGTTAGGA GAGATTGGAG ACGGAGATGT ATGAAATTCC ATAAGGCGAT TGGAGAACCA TGGGACATTT GTGAGGAAAT GGCCAATICI TTCCTGGCTT AACATTAAAA AATCC // TTACATGAGT TACAGAAAGG AGCTGCTAAA GGAGTTAAAA AATGAAGGAA ACTCAAGATC CATAAATTCA AAGCTCCCTG ACGAAGAAGA ATACTAAAAC CTTGCCAATT CGATGGTCCA ATTAGCAATA GAATATTACA CCAAGTCTCT AAAACTCTTA GCAAATTCTT GAAAGTTTG GGAGGAGAAA ATTCTTCGTT TTTGGAGACA AACAAGACCA TGGTTTTATA GGAGCTCGAA AATACAAAAG GTATGACGCA GGGATTTGGA AACTATCCCA TTAAGACAAA AAAAAGCGAT ATGAGCAGAT TCGGCCTAAC AGGACATCCC TAAAAGAAGT CAAAGAAACT GATGGTACTG GTCTCTATGC ATAAGAGGG TCATTACTCG AAGCTAGAGT TAAATCTTGA TAGTATGGAA TTGTAAAATA TACTTAGAGG AAAAGCACAA GGATATTGGA CTCGCAATAT TACGATCCCA ACAAGACAAG CTCAGGGAGA ATAGTATACC AGACAAAAGA GCTCTAGAAT CCCGATACTC GACTATAGAC TACATCGAGT GACACTGATG GAAGGGTTTT GAAGGAAAAG GTGAGAATAG GTAGCTGTTG GGATACATAG AAGTTCTGCA GCAAAAGCAA AAAGAAACTC GCGGTACTTA

TGA

Figure 17WW

KOD DNA POLYMERASE - Sac7d fusion protein [Fig.17-WW]

Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 34) // Nucleotide sequence (SEQ ID NO: 69)

CGT (ALL POSSIBLE CODONS FOR ARGININE) GTCAAGAAGA TAACCGCCGA GAGGCACGGG ACGGITGIAA CGGIIAAGCG GGIIGAAAAG GIICAGAAGA AGIICCICGG GAGACCAGII CAGCGATAAG GGACAAGATA CTGTCATAAG AATTTTCAAG CTTCTACGCC V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) TTGAACCCTA SAGGICIGGA AACICIACII TACICAICCG CAGGACXXXC ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GCGAGTTTAA GATTGAGTAC GACCGGACTT CATTGAGGAA ACGATTCTGC CTCCTGAAGG AAGGAAAACG

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TIT ACC TAT GAC GAC
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              GGCGACGAGG AGCTGAAAAT
                                              ATAACTTGGA AGAACGTGGA
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                               GACATTGAAA
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ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

GAC

TTA

AAT GGT

Figure 17XX

Sac7d - kod dna polymerase fusion protein [Fig.17-XX]

Nucleotide sequence (SEO ID NO: 69) // Nucleotide sequence (SEQ ID NO: 33) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 34) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAA //

1020 CCTCAGGAAG 1080 1140 //ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60 480 540 009 CTCCTGAAGG ACGATTCTGC CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG 180 AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120 CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG GAGACCAGTT 240 CGTTTATGAA 840 GGACAAGATA AGCCTGGGAA CGGCCAGTCC GGCCAGAAGA GGAGAACATA GIGIACCIAG AITITAGAIC CCIGIACCCC ICAAICAICA ICACCCACAA CGICICGCCG CAAGCGCTAC TCTCCCCTAC CTTCGATCTC GGTCACATAC CCTTATGATA GCTCGCCTTC CTATCTGAAA CGAGCCGAAG TGTGAAGGAG TGAGGGCGAG GAGTTCGCCG AGGGGCCAAT CGGCAGAGCT ATGAAGGAGG CTATGTAAAA GAGCCCGAGA GAGGGTTGTG CCCACATACA CGCTTGAGGC GAGGICIGGA AACICIACII TACICAICCG CAGGACXXXC CAGCGATAAG CAGCAGTIAT IGACATCIAC GAGTACGACA TACCCTICGC GCCAATGGAA GGCGACGAGG AGCTGAAAT GGCCAGGGTG ATAACTTGGA AGAACGTGGA GAGGGAGATG ATAAAGCGCT TCCTCCGTGT GTTTGCCGTC GAAGTGAAGG GACGGATACA GGAGAAGGIT TACGCTGAGG AAATAACCAC TACTCGATGG AAGATGCGAA GCCCAGCTTT CTCGCTTAAT CAGCACTGGC AACCTCGTTG AGTGGTTCCT GGCCCCGAAC AAGCCCGATG AAAAGGAGCT TCGACTTCGC GGGATGGAAG AATAAACTTC GCCCTCGGAA AACCTACAAC GGCGACAACT GATAAACCTG AGTCGCCCGC TCCGATGGAG ACGTICICAL GTCAGCCGAA AGGGATTAGT CTCTCTACCA ACGAGGAAGG AAAAGCTCGG TGGGCGACAG TAAGACGGAC ACCTTGAGAG TCTCCCGCTC GGAATGAGCT TCTCGACGGA AGGAGTTCCT ACGGTTGTAA CTCATAGACA AAAGACCCGG TATCCTGTGA ACCGGCGAGA CTCTGGGACG GCCTATGAGA CGAGAGCATC GACATTGAAA AGCTACGCCG AAGCGCTGTG ATTCAGAGGA GCCGTCTTCG GAGCTTGGGA GTTGACGTCG

1440 1500 1560 1620 1680 1740 1800 1860 1920 1980 2040 2100 2160 1380 2220 AGAGGAGAGG AAGGGAGTAC CTACAGCGAC GIGAGGCGIG ACTGGAGCGA GATAGCGAAA GTGACGTCGA GAAGGCCGTG GCCCTGGAAC GGTGATAAGC CGATACCGTT CGACGAGTTC CGGCCACCGC GCTCCTCGAT AAAGAAGGCT CGAGTACGAG GGAGAAGCTG CGACGCCGAG TACTACATTG AGAACCAGGT TCTCCCAGCC CGCAAGGAAG ACCTGCGCTA CCAGAAGACG CGGCTATGCA AGACGAGGAA TCCCCACGTT AGACAGGITG GITIGAGIGC IIGGCIGAAG CCGAAGGGAA CI //IAG 2325 CGGCCTGGGG AATACCTGGA GCCGATGCTG AAACCGTCAA CCCCACAGGT GAGACCTCCT TCGAGAGGAA ACGGTTACTA TTAAGGTAAT ATGCGGTGAT AGGCAACCGG CGCTTGAGCT AGGTTCCGCC TATGACGTTG GAAGGCCACG ATTGACCCGA AGCAAGTACG AACAGCTACT AAGTACGGCT CTTCCGGGCG AAGAAGAAGT CTAAAGGACG AAGGACTACA GGCGACAGGG TICTGCAAGG ACTICCCAGG AITIAICCCG AGCCIGCIIG GGAGTGTGCA GAGAGCGTAA GTCAAAATAC GATCCTGGCA GATAGAGGAA ACAGAGAAGG ATGCAAGGAA CGAAAAGCTG GAGGGATTTA CAACGCCAAA CTTCGTCACG ACTTGAGATT TGAAGCTTTG TGGGAGGATA CGCGAGAGGA CTTCGGTTAC AGAAGAAGAT TTTTTGCCAC CAACGCGCGG GGGCCATCAA GGTACTGCAA CCATCAAGGA TCAAGTATAT AACGCGGCTT CGAGGGTTCT AAGAAGTTAC AGCAGATAAC AGAGGTTGGC TCAAGGGCTC AGCACAAGTA TTCTGAGAGC GATACGCTCA GTTGAGAGAA AGGCGCGCT GTGATCCACG TACATCGTGC CAGAAGATAA ATGGAGTTCC GGCTTCTACA GGCAAGATAA GAGACGCAGG AGGATAGTCA GCCGTTGCCA GACCCGACGA TACAGGCAGA ATAACGATGA ACCGACGGAT

Figure 17YY

Sac7d-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17-YY]

// Nucleotide sequence (SEQ ID NO; 36) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 69) V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

AAAGAGAACG GGGAGTTTAA AATAGAACTT GACCCTCATT TTCAGCCCTA TATATATGCT 120 ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG 60

CTTCTCAAAG	ATGACTCCGC GAGTGCTCGA	TATTGAGGAG TGCAGTGAAA	ATAAAGGCAA GTCAGGAAAA	TAAAGGGCGA	GAGACATGGA AAGGGAAGTT	
SAAGTCTGGA	AGCTCATTTT	CGAGCATCCC	CAAGACXXXC GAATATGACA	CAGCTATGCG TACCCTTTGC	GGGCAAAATA CAAGCGTTAT	300 360
CTCATAGACA	AGGGCTTGAT	TCCCATGGAG	GGAGACGAGG	AGCTTAAGCT	CCTTGCCTTT	
SATATTGAAA	CGTTTTATCA	TGAGGGAGAT	GAATTTGGAA	AGGGCGAGAT	AATAATGATT	480
AGTTATGCCG	ATGAAGAAGA	GGCCAGAGTA	ATCACATGGA	AAAATATCGA	TTTGCCGTAT	540
STCGATGTTG	TGTCCAATGA	AAGAGAAATG	ATAAAGCGTT	TTGTTCAAGT	TGTTAAAGAA	
AAAGACCCCG	ATGTGATAAT	AACTTACAAT	GGGGACAATT	TTGATTTGCC	GTATCTCATA	099
AAACGGGCAG	AAAAGCTGGG	AGTTCGGCTT	GTCTTAGGAA	GGGACAAAGA	ACATCCCGAA	720
CCCAAGATTC	AGAGGATGGG	TGATAGTTTT	GCTGTGGAAA	TCAAGGGTAG	AATCCACTTT	780
SATCTTTTCC	CAGTIGIGGG	AAGGACGATA	AACCTCCCAA	CGTATACGCT	TGAGGCAGTT	840
TATGAAGCAG	TTTTAGGAAA	AACCAAAAGC	AAATTAGGAG	CAGAGGAAAT	TGCCGCTATA	006
TGGGAAACAG	AAGAAAGCAT	GAAAAAACTA	GCCCAGTACT	CAATGGAAGA	TGCTAGGGCA	096
ACGTATGAGC	TCGGGAAGGA	ATTCTTCCCC	ATGGAAGCTG	AGCTGGCAAA	GCTGATAGGT	1020
CAAAGTGTAT	GGGACGTCTC	GAGATCAAGC	ACCGGCAACC	TCGTGGAGTG	GTATCTTTA	1080
AGGGTGGCAT	ACGCGAGGAA	TGAACTTGCA	CCGAACAAAC	CTGATGAGGA	AGAGTATAAA	1140
CGCCCTTAA	GAACAACTTA	CCTGGGAGGA	TATGTAAAAG	AGCCAGAAAA	AGGTTTGTGG	1200
SAAAATATCA	TTTATTTGGA	TTTCCGCAGT	CTGTACCCTT	CAATAATAGT	TACTCACAAC	1260
STATCCCCAG	ATACCCTTGA	AAAAGAGGGC	TGTAAGAATT	ACGATGTTGC	TCCGATAGTA	1320
GGATATAGGT	TCTGCAAGGA	CTTTCCGGGC	TTTATTCCCT	CCATACTCGG	GGACTTAATT	38
SCAATGAGGC	AAGATATAAA	GAAGAAAATG	AAATCCACAA	TTGACCCGAT	CGAAAAGAAA	1440
ATGCTCGATT	ATAGGCAAAG	GGCTATTAAA	TTGCTTGCAA	ACAGCTATTA	CGGCTATATG	1500
GGGTATCCTA	AGGCAAGATG	GTACTCGAAG	GAATGTGCTG	AAAGCGTTAC	CGCATGGGGG	1560
AGACACTACA	TAGAGATGAC	GATAAGAGAA	ATAGAGGAAA	AGTICGGCTT	TAAGGTTCTT	1620
TATGCGGACA	CTGACGGCTT	TTATGCCACA	ATACCCGGGG	AAAAGCCTGA	ACTCATTAAA	1680
AAGAAAGCCA	AGGAATTCCT	AAACTACATA	AACTCCAAAC	TTCCAGGTCT	GCTTGAGCTT	1740
SAGTATGAGG	GCTTTTACTT	GAGAGGATTC	TTTGTTACAA	AAAAGCGCTA	TGCAGTCATA	1800
GATGAAGAGG	GCAGGATAAC	AACAAGGGGC	TTGGAAGTAG	TAAGGAGAGA	TTGGAGTGAG	1860
ATAGCTAAGG	AGACTCAGGC	AAAGGTTTTA	GAGGCTATAC	TTAAAGAGGG	AAGTGTTGAA	1920
AAAGCTGTAG	AAGTTGTTAG	AGATGTTGTA	GAGAAAATAG	CAAAATACAG	GGTTCCACTT	1980
GAAAAGCTTG	TTATCCATGA	GCAGATTACC	AGGGATTTAA	AGGACTACAA	AGCCATTGGC	04
CCTCATGTCG	CGATAGCAAA	AAGACTTGCC	GCAAGAGGGA	TAAAAGTGAA	ACCGGGCACA	2100
ATAATAAGCT	ATATCGTTCT	CAAAGGGAGC	GGAAAGATAA	GCGATAGGGT	AATTTTACTT	2160
ACAGAATACG	ATCCTAGAAA	ACACAAGTAC	GATCCGGACT	ACTACATAGA	AAACCAAGTT	7
TTGCCGGCAG	TACTTAGGAT	ACTCGAAGCG	TTTGGATACA	GAAAGGAGGA	TTTAAGGTAT	2280
CAAAGCTCAA	AACAAACCGG	CTTAGATGCA	TGGCTCAAGA	GGTAG 2325		

Figure 1727

Vent DNA POLYMERASE - Sac7d FUSION PROTEIN [Fig.17-ZZ

// Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEO ID NO; 69) Nucleotide sequence (SEQ ID NO: 35) Nucleotide sequence (SEQ ID NO: 36)

CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID) CGG, cec, CGA, = AGA, AGG, V93R MUTANT: XXX

1140 1020 1080 780 840 900 480 540 900 9 GGGCAAAATA GTATCTCATA TGAGGCAGTT TGCCGCTATA GTATCTTTA AGAGTATAAA CTATAATCCG AATTTTAAG TATATACCT GAGACATGGA AAGGGAAGTT CAAGCGTTAT CCTTGCCTTT AATAATGATT TTTGCCGTAT TGTTAAAGAA ACATCCCGAA AATCCACTTT TGCTAGGGCA GCTGATAGGT AGGTTTGTGG TACTCACAAC TTCAGCCCTA CAGCTATGCG AGGGCGAGAT TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA CCTGGGAGGA TATGTAAAAG AGCCAGAAAA CAATAATAGT AATTTTGGG TACCCTTTGC AAAATATCGA TTGATTTGCC AGCTGGCAAA TCGTGGAGTG CTGATGAGGA TAAAGGGCGA AGCTTAAGCT GAATATGACA GGAGACGAGG GAATTTGGAA AAGAGAAATG ATAAAGCGTT GGGGACAATT AACCAAAAGC AAATTAGGAG ACCGGCAACC CTGTACCCTT ACACTGATTA CATAACAAAA GATGGCAAGC GACCCTCATT ATAAAGGCAA GTCAGGAAAA CAAGACXXXC ATCACATGGA GTCTTAGGAA GCTGTGGAAA AACCTCCCAA GCCCAGTACT ATGGAAGCTG CCGAACAAAC CGAGCATCCC GAAAAAACTA ATTCTTCCCC GAGATCAAGC TGAACTTGCA TTTCCGCAGT AATAGAACTT TATTGAGGAG TGACATTTAC TCCCATGGAG TGAGGGAGAT GGCCAGAGTA AACTTACAAT AAGGACGATA TGCAGTGAAA AGTTCGGCTT TGATAGTTT GGGAGTTTAA ATGACTCCGC AGGCCTTGAT CGTTTTATCA TGTCCAATGA ATGTGATAAT AGAGGATGGG CAGTTGTGCG TTTTAGGAAA TCGGGAAGGA GAACAACTTA TTTATTTGGA GAGTGCTCGA AGCTCATTTT CAGCTGTGGT ATGAAGAAGA AAAAGCTGGG AAGAAAGCAT GGGACGTCTC ACGCGAGGAA CTTCTCAAAG AGGGTGGCAT GAAAATATCA ATGATACTGG GAAGTCTGGA CTCATAGACA AAAGACCCCG AAACGGGCAG GATCTTTCC TATGAAGCAG TGGGAAACAG CAAAGTGTAT CGGCGCTTAA AAAGAGAACG AAAACTGTGA AGGGAACATC GATATTGAAA AGTTATGCCG GTCGATGTTG CCCAAGATTC ACGTATGAGC

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1500
                                                                   1620
                                                                                 1680
                                                                                               1740
                                                                                                            1800
                                                                                                                         1860
                                                                                                                                                    1980
              1380
                           1440
                                                      1560
                                                                                                                                      1920
                                                                                                                                                                  2040
                                                                                                                                                                                2100
                                                                                                                                                                                              2160
TCCGATAGTA
              GGACTTAATT
                                                                                                                         TTGGAGTGAG
                                                                                                                                     AAGTGTTGAA
                                                                                                                                                                                             AATTTTACTT
                           CGAAAAGAAA
                                                     CGCATGGGGG
                                                                                 ACTCATTAAA
                                                                                             GCTTGAGCTT
                                                                                                                                                   GGTTCCACTT
                                                                                                                                                                 AGCCATTGGC
                                        CGGCTATATG
                                                                    TAAGGTTCTT
                                                                                                           TGCAGTCATA
                                                                                                                                                                                ACCGGGCACA
                                                                                                                                                                                                           AAACCAAGTT
                                                                                                                                                                                                                          TTTAAGGTAT
                                                                                                                                                                 AGGACTACAA
                                                                                                                                                                                             GGAAAGATAA GCGATAGGGT
ACGATGTTGC
                                                                               AAAAGCCTGA
                                                                                                                         AACAAGGGC TTGGAAGTAG TAAGGAGAGA
                                                                                                                                      TTAAAGAGGG
                                                                                                                                                    CAAAATACAG
                                                                                                                                                                                TAAAAGTGAA
                                                                                                                                                                                                           ACACAAGTAC GATCCGGACT ACTACATAGA
                                                                                                                                                                                                                         TTTGGATACA GAAAGGAGGA
              CCATACTCGG
                          TTGACCCGAT
                                                      AAAGCGTTAC
                                                                                             TTCCAGGTCT
                                         ACAGCTATTA
                                                                    AGTTCGGCTT
                                                                                                           AAAAGCGCTA
                                                                                                                                                                                                                                      CTTAGATGCA TGGCTCAAGA GG 2325 //
TGTAAGAATT
                          AAATCCACAA
                                                                                                                                     GAGGCTATAC
                                                                                                                                                                 AGGGATTTAA
                                         TTGCTTGCAA
                                                      GAATGTGCTG
                                                                                                                                                                                GCAAGAGGGA
                                                                    ATAGAGGAAA
                                                                                 ATACCCGGGG
                                                                                             AACTCCAAAC
                                                                                                            TTTGTTACAA
                                                                                                                                                    GAGAAAATAG
              TTTATTCCCT
                                                                                             AAACTACATA
                                                                                                                                                    AGATGTTGTA
                                                                                                                                                                                             CAAAGGGAGC
                                                                                                                                                                                                                        ACTCGAAGCG
              CITICCGGGC
                           GAAGAAAATG
                                                                                 TTATGCCACA
AAAAGAGGGC
                                         GGCTATTAAA
                                                      GTACTCGAAG
                                                                     GATAAGAGAA
                                                                                                           GAGAGGATTC
                                                                                                                                      AAAGGTTTTA
                                                                                                                                                                 GCAGATTACC
                                                                                                                                                                                AAGACTTGCC
                                                                                                                                                                                                                                      AACAAACCGG
ATACCCTTGA
                                                                                                                                                    AAGTTGTTAG
                                                                                                                                                                                                            ATCCTAGAAA
                                                                                                                                                                                                                          TACTTAGGAT
                                                                                                                         GCAGGATAAC
                                                                                                                                      AGACTCAGGC
                                                                                                                                                                 TTATCCATGA
                                                                                                                                                                                CGATAGCAAA
                                                                                                                                                                                              ATATCGTTCT
                          AAGATATAAA
                                                      AGGCAAGATG
                                                                                              AGGAATTCCT
              TCTGCAAGGA
                                         ATAGGCAAAG
                                                                    TAGAGATGAC
                                                                                 CTGACGGCTT
                                                                                                            GCTTTTACTT
STATCCCCAG
                                                                                                                                                                                                           ACAGAATACG
                                                                                                                                                                                                                                        CAAAGCTCAA
              GGATATAGGT
                          GCAATGAGGC
                                                                                                                                                    AAAGCTGTAG
                                                                                                                                                                                             ATAATAAGCT
                                                                                                                                                                                                                          TTGCCGGCAG
                                                                                             AAGAAAGCCA
                                                                                                                         GATGAAGAGG
                                                                                                                                      ATAGCTAAGG
                                                                                                                                                                                CCTCATGTCG
                                                      GGGTATCCTA
                                                                                 TATGCGGACA
                                                                                                                                                                   GAAAAGCTTG
                                         ATGCTCGATT
                                                                    AGACACTACA
                                                                                                            GAGTATGAGG
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GAC TTT ACC TAT GAC GCT CCA AAA GAA GTA GAC ACT GAA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC GGA GCT GTA AGC GAG AAA GAT GAA GAG AAA GCA GAA AGA GAG AAG AAA // AAG GTA AAG TTC AAG TAT AAG GGT AAG ACA GGT AGA ATG TTA GCA AGA AAT GGT AAG ATA TTA GAC // ATG GTG

Figure 17AAA

Deep Vent- Sac7d DNA polymerase fusion protein [Fig.17-AAA]

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide seguence (SEQ ID NO: 37) // Nucleotide seguence (SEQ ID NO: 69)

2220 2280 2328 2160 GGCTACATAG TGCTGAGGGG AGACGGGCCA ATAAGCAAGA GGGCTATCCT TGCAGAGGAG TTCGATCTCA GGAAGCATAA GTATGACGCT GAGTATTACA TAGAAAATCA GGTTTTACCT GAATATTAGA GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG ACTAAACAGA CAGGTCTTAC GGCATGGCTT AACATCAAGA AGAAG // GCCGTTCTTA

TCA TIT ACC TAT GAC GAC GCT CCA AAA GAA TTA GAA GTA GAC ACT TGA GAA GAG AAA AGA GTA GGC AAA ATG GTG TCC GGA GCT GTA AGC GAG AAA GAT GCA GAA AGA GAG AAG AAA // AAG TAT AAG GGT GTA AAG TTC TTA GAC ATG TTA GCA AGA AAG ATA AAG AAG GTT TGG AAT GGT AAG ACA GGT AGA AAG // ATG GTG

Figure 17BBB

Sac7d - Deep Vent DNA polymerase fusion protein [Fig.17-BBB]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 37)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

// ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

180 240 300 360 420 480 540 909 //ATGATACTTG ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG GATTTTCAAG AAAGAAAACG GCGAGTTTAA GGTTGAGTAC GACAGAAACT TTAGACCTTA CATTTACGCT CTCCTCAAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA GAGGCATGGG GAGGCCGATT TGACATCTTT GAGTACGACA TTCCGTTCGC GAAGAGGTAC TATAATGATA TITCCAGCGA GAGGGAGATG ATAAAGCGGT TCCTCAAGGT GATAAGGGAG GGATAAGATA GCTCGCATTT TGAACACCCT CAGGACXXXC CCGCAATAAG TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG TCCAATGGAA GGCGATGAAG AGCTCAAGTT CGAAGGGAG GAGTTCGCGA AGGGGCCCAT AGCCAAAGTC ATAACGTGGA AAAAGATCGA AAGGCCTAAT ATGAGGAAGA GAATTATAGA GGCTGTACTT CCCTCTATCA CCGCAGTTAT STCGAGGTAG GACATAGAAA AGCTATGCTG AGAGAGCATT CTAATAGACA GAGGTATGGA AAGATAGTGA

AAAGATCCCG	ATGTTATAAT	TACCTACAAC	GGCGATTCTT	TCGACCTTCC	CTATCTAGTT	099
ĸ,	AAAAGCTCGG	GATAAAGCTA	CCCCTGGGAA	GGGACGGTAG	TGAGCCAAAG	720
_	TTGGGGATAT	GACAGCGGTG	GAGATAAAGG	GAAGGATACA	CTTTGACCTC	780
Н	LTAGGAGAAC	GATAAACCTC	CCAACATACA	CCCTCGAGGC	AGTTTATGAG	840
O	GAAAGCCAAA	GGAGAAAGTT	TACGCTCACG	AGATAGCTGA	GGCCTGGGAG	900
\mathbf{c}	GACTGGAGAG	AGTTGCAAAG	TATTCAATGG	AGGATGCAAA	GGTAACGTAC	960
$\overline{}$	GGGAGTTCTT	CCCAATGGAG	GCCCAGCTTT	CAAGGTTAGT	CGGCCAGCCC	1020
	TTTCTAGGTC	TTCAACTGGC	AACTTGGTGG	AGTGGTACCT	CCTCAGGAAG	1080
\sim	GGAATGAATT	GGCTCCAAAC	AAGCCGGATG	AGAGGGAGTA	CGAGAGAAGG	1140
	GCTACGCTGG	GGGATACGTT	AAGGAGCCGG	AGAAAGGGCT	CTGGGAGGGG	1200
	TAGATTTCAG	GAGCCTGTAC	CCCTCGATAA	TAATCACCCA	TAACGICICA	1260
	TGAACAGGGA	AGGGTGTAGG	GAATACGATG	TCGCCCCAGA	GGTTGGGCAC	1320
	AGGACTTCCC	GGGGTTTATC	CCCAGCCTGC	TCAAGAGGTT	ATTGGATGAA	1380
	TAAAAAGGAA	GATGAAAGCT	TCTAAAGACC	CAATCGAGAA	GAAGATGCTT	1440
	AACGGGCAAT	CAAAATCCTG	GCAAACAGCT	ATTATGGGTA	TTATGGGTAC	1500
	GTTGGTACTG	TAAGGAGTGC	GCAGAGAGCG	TTACGGCCTG	GGGGAGGGAA	1560
	TCGTAAGGAA	GGAACTGGAG	GAAAAGTTCG	GGTTCAAAGT	CTTATACATA	1620
	GACTCTACGC	CACAATTCCT	GGGGCAAAAC	CCGAGGAGAT	AAAGAAGAAA	1680
	TCGTAGATTA	TATAAACGCC	AAGCTCCCAG	GGCTGTTGGA	GCTTGAGTAC	1740
	ACGTGAGAGG	GTICTICGIG	ACGAAGAAGA	AGTATGCGTT	GATAGATGAG	1800
	TAATCACTAG	GGGGCTTGAA	ATAGTCAGGA	GGGACTGGAG	CGAAATAGCC	1860
	AAGCAAAAGT	CCTAGAGGCT	ATCCTAAAGC	ATGGCAACGT	TGAGGAGGCA	1920
	TTAAGGAGGT	AACTGAAAAG	CTGAGCAAGT	ACGAAATACC	TCCAGAAAAG	1980
	ACGAGCAGAT	CACGAGGCCC	CTTCACGAGT	ACAAGGCTAT	AGGTCCGCAC	2040
	CAAAAAGGTT	AGCCGCTAGA	GGAGTAAAGG	TGAGGCCTGG	CATGGTGATA	2100
	TGCTGAGGGG	AGACGGGCCA	ATAAGCAAGA	GGGCTATCCT	TGCAGAGGAG	2160
	GGAAGCATAA	GTATGACGCT	GAGTATTACA	TAGAAAATCA	GGTTTTACCT	2220
	GAATATTAGA	GGCCTTTGGG	TACAGGAAAG	AAGACCTCAG	GTGGCAGAAG	2280
	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAG TAA		2328

Figure 17CCC

JDF-3 - Sac7d fusion protein [Fig.17-CCC]

Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 69) Nucleotide sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 69)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTCGAGATCGAGACGCTCTACCACGAGGGAGAGAGTTTGGAA acgecegregetracetrangeragecegragecegracetrangeraratarecrange entrecragecetrange entra de la comparcace de la comparce del comparce de la comparce de la comparce de la comparce de la comparce del comparce de la comparce del la comparce de la compa ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGCTTTGAGAG CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAATCTCCTCGATTACAGGCCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT GAACTCGAATACGAGGCCTTCTACGTCAGGGGCTTCTTCGTCACGAAAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGC GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAg< CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC a cococtica do de la composa d CAGGTCTGTGGAGGTCTGGGTCCTCTACTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATACCC GCGCTTCTTGAGGGTCGTTAAGGAGGAGCCCGGACGTGCTGATAACATACAACGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCCTTGGCGTTGGCGTTTG acceticggagggagggagggaggtgagatacagcgcatgggggacaggtttgcggtcgaggtgaagggcagggtacacttcgacctttatecagtcataaggcgcaccataa GTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGGGAAAAGTTCGGTTTTAAAGTCCT CTATGCAGACAGACGGTCTCCATGCCACTTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC atigaagcgagatagcgaaggggagaggggagggttttggaggcgatactcaggcacggtgacgttgaagaggccgtcagaattgtcagggaagtcaccgaaaagctgagcaa A TO THE ACCITICATIVACATICA COCAGA A TIGGAA A GCCC GTICA TICA GGG TICTICA A GGA GGA GGA GGTICA GGA TITICA A TA GTGGCTGAAGCCGAAGGGGAAGAAGAAG/

AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA // TAG

Figure 17DDD

Sac7d - JDF-3 fusion protein [Fig.17-DDD]

Nucleotide sequence (SEQ ID NO: 69) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEO ID NO: 69) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

AAG ATA AAG AAG GTT TGG AGA GTA GGC AAA ATG GTG TCC TTT ACC TAT GAC GAC AAT GGT AAG ACA GGT AGA GCT GTA AGC GAG AAA GAT GCT CCA AAA GAA TTA // ATG GTG AAG GTA AAG TTC AAG TAT AAG GGT GAA GAG AAA GAA GTA GAC ACT TCA TTA GAC ATG TTA GCA AGA GCA GAA AGA GAG AAG AAA //

ccrrceccaaececracercaragacaaaggeccraarecegaregaaggraggaaggerraaacrearerecrrdgadardgadgacecreraecacgagggagaagagr GGCAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGTCTCCTCGATTACAGGCAACGGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGG CTACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTJTCAATCATCACCCACACACGTCTCGCCAGAT **GGCAGGTCTGTGGAGGTCTTGGGTCCTTTCACGCACCCGCAGGACXXX**CCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATAC TTACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACCAT AAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCGGCGAGGGGGCTTGAG ACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCCCGAGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGCTCGAAACCTGCTGGAGGAAA CTATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTC CGACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGC STGTTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGACGACGACGACGAAGCACAAGTACGA //ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTACTT CTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGGAGAAGGTGAAAAAAGTTCCTC AAGCGCTTCTTGAGGGTCGTTAAGGAGGACCCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGAGCT AGGGTCGCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTT CTCTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTC TCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCG

Figure 17EEE

Synthetic Sso7d gene [Fig. 17-EEE]:

Nucleotide sequence (SEQ ID NO: 71) Amino acid sequence (SEQ ID NO: 72)

ဗ္ဗဗ္ဗ A T V K F K Y K G E E K E V D I S K GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG I K K V W R V G K M I S F T Y D E ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG

G G K T G R G A V S E K D A P K E L GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L Q M L E K Q K K CTG CAG ATG CTG GAG AAG CAG AAA AAG

Figure 17FFF

Sso7d-Taq DNA polymerase fusion protein [Fig.17-FFF]

Amino acid sequence (SEQ ID NO: 72) // Amino acid sequence (SEQ ID NO: 66) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 65)

// A T V K F K Y K G E E K E V D I S K // GCA ACC GTA AAG TIC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG

I K K V W R V G K M I S F T Y D E G ATC ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC G G K T G R G A V S E K D A P K E L GGT GGC AAG ACC GGC CGT GCT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG

L Q M L E K Q K K // G G G CTG CAG ATG CTG GAG AAA AAG // GGC GGC GGT

Marked-Up Version

GGG V GTG T မှ ငြင် P CCA r CTG A A A Y W K AAG E CTG ч Н CTG r CTG T ACC TACG S AGC GAC A GCC ი მვვ CAG V GTC I r G r CTC A GCC K S AAG AGC C CCC CIC CTC CTC K AAG A GCC E GAG GAC ი მვვ S AGC K AAG œ D A GAC GCC D GAC V GTC g GGC A GCC CTG T ACC r CCC CCC P CCC ი გე E GAG R V GTG V GTC k AAG R CGG CIC CAC R AGG W CGG LCTT A GCC × K G AAG GGC V F GTC TTT A GCC GCC D D GAC GAC r CTG L CTG IATC CTC L CTG N AAC E I ATC F TTC (GAG g G C C CGC R V GTC ဗ္ဗဋ္ဌ DGAC E gcc Gcc 田 ဗ ညဗ္ဗ H L I K CTC ATC AAG C CCC G Y K G Y E A V I V GTG ATC GTG V GTC Y CAC CAC S TCC မှ ည r CTG Y TAC E GAG K AAG F E I ATC E K AAG CTT [X]<u>V</u> [0]<u>G</u>TC 3 F TTT T ACC Y R GAA DGAC K AAG r CTG ß CTC A GCG ი ცცც A GCG A GCC ဗ္ဗဋ္ဌ DGAC ₩ TGG R AGG CGG GGC ය ශ්රී ᆸ GC P DGAC Y TAC CIC CCG Y c SG E GAG s TCC L T ACC A GCG D GAC ¥ ი წმშ CAA V GTC r CTG A GCC A GCC K AAG Γ W TGG L CTG V GTG r CTG T ACG ы E GAG R CGG E M ATG r CTG P CCG GAC E GAA CŢĊ A GCC A GCC K AAG N AAC Д ი ცვვ CIC H CAC E GAG E GAG H P A GCG CAG P E K AAG R CGG Д K AAG GGC r CTC CAC ი მვვ ය දු F AAG Y T ACC Y ი წვვ CIC GAC A GCG K AAG I ATC DGAC CTC TACT ဗ ည် R GG F $_{
m CTT}$ IATC Ħ v GTC ဗ္ဗဗ္ဗ A GCC DGAC S TCC E L GAC LCTC GCC s AGC A GCC A GCC

Marked-Up Version

GAC A 3CC A 3CC G F ස පු IATC L A A V GTG r H r E ACC r CTG X X V GTT CTC Y IAC L Y FAC R AGG ဗ္ဗဋ္ဌ ၁ ဗို G GGG E r CHO CGC E R GAG AGG L CTC R L F E GAA L Y TAT s AGC ACG AAC AAC E CCG D GAT L M ATG ශ රයිය W TGG A GCC 3CC $^{
m F}$ ۳ کا کاری PCCT AAG E DGAC P S TCC LCTT DGAC H မှ ည A A GCC E GAG V GTG GCC DGAC G G G r CTC CCC W TGG က် ကို K AAA V GTG LCTT LCTC M ATG E CAC CTG ¥ 5 TGG M ATG A GCC A GCC D ი მმმ A GCC CAC မ မရှင် E L R AGG r CTG TGG GAC CIC g ggc E g G G gg A R S AGC GCC CCC မှ ည R A GCC E s Icc ဗ္ဗဗ္ဗ E CAC L မှ R CGG L R AGG g G G CCC E GAG L ITG r. CTG TCC K AAG E E V GTC . 366 P CCG T ACC ი მვმ V GTC RGC AAA AAA F TTT A GCC ACC CICR GGG E AGCT F TTC A GCC E E R ж С L ი მვვ R AGG CTG AAG N AAC F L န ၂၄၄ ဗ္ဗဋ္ဌ A 3CG ဗ္ဗဗ္ဗ A GCG L S CTC V GTC CTT s TCC L E D GAC A CTT ი მვვ E R AGG LCTT Y TAT R AGG EGAG GAT PCCT V GTG E K AAG V GTG R AGG K AAG ဝ ၁၁၅ E g ggg P A GCC A GCC GAC E မှ ငြင်င A 3CC L DGAC T ACG ¥ TGG R AGG r F E V GTG E GAG ATG r CTG s AGC ဗ္ဗဋ္ဌ A 3CC D R AGG r CTG W TGG r CTG E DGAC r G F TTT E N AAC V GTG မှ ည g G C C E GAA V GTG A R AGG r CTG r CTC L R F r CTG L Y TAC R AGG L A GCC 3CC E gg Gg A GCC L ი მმმ

Marked-Up Version

A GCC ACC. R AGG Y TAT IATC T ACG S AGT IATC F I ATC A P Y E o CAG CIA A GCC r CTC R AGG CIA DGAC r CTG M ATG ACC ACC F . 366 က ည L CTG GAG CCC ი მვვ CTG W TGG E s AGC R AGG N AAC K AAG R CGG CTT V GTC R CGG CAC ය යි L gcc Gcc E s AGC A GCC CAG CAG Q CAG R AGG I ATC g GGG A GCC Y A GCG S TCC F TTT T ACG P CCG V GTG D GAC 4 9 R AGG CTA A GCC o CAG r CTC A GCC T ACC $_{
m LTG}$ g GGC T ACC R CGG r CTC Y TAC ය ශීරී GAG CTG s AGC D GAC GGC CGC LCTA s TCC GAG GGC RCGC r CGC E ССА T ACG T I ATC P ACG M ATG A GCC V GTC W TGG CIC H E GAG F TTT S TCC AAG $_{
m LTG}$ CCC ი მვვ CAC CAC L CTG A GCC I ATT TAC T ACG CIG × GAG CCC r CTC CAG F GGC CGC R CGC I ATC E GAG A GCC IATC P S TCG ACC N AAC E V GTG GAC N AAC GGC V GTC K AAG DGAC D GAC r CTG M ATG A GCC K AAG A GCC I ATC I ATT g GGC ${
m F}$ Q CAG V GTG R CGG V GTG g GGC o CAG E GAG GAA P Y TAC යිය ACC Y TAC CIC I ATC A GCC GGC GC ი ცვ A GCC I ATT R AGG ⊢ T ACC CTG AAG F r CTC E H T ACC AAC AAC CIC E GAG GAG ¥ N F × T L ACC CTC CAG GAG A GCC s AGC H CAC GCC A GCC GAG CAG R V GTC E A GCC 田 P CCC ი მვვ Y TAC R CGG TACG E K AAG L DGAT CGG I ATA F PCCT GTG GAG CGG K AAG R r CTG R S TCC r GGC CAG V GTC V GTC F TTC V GTG s AGC N AAC ATC s AGC IATC R CGG ဗ္ဗဋ္ဌ န Icc ဗ္ဗဗ္ဗ CTC K AAG ဗ္ဗဗ္ဗ H

g GGC P V CCC GTC C M ATG (F N TTC AAC 1 A E R M A GCC GAG CGC ATG GCC ₽ B R E CGG GAG (VGTG K S AAG AGC (

E CTG R AGG CCC \mathbf{F} CTC K AAG V GTG M ATG L A CTG GCT L M K CTC ATG AAG DGAC gcc Gcc T A ACC GCC

A L E CTC GAG V GTC L CTG D E GAC GAG H L Q V CTT CAG GTC (r CTC R M AGG ATG C GGG GCC E M GAA ATG

G GGG P K E R A E A V A R L A K E V M E CCA AAA GAG AGG GGG GAG GCC GTG GCC CGG CTG GCC AAG GAG GTC ATG GAG

W TGG H V Y P L A V P L E V E V G I G E D GTG TAT CCC CTG GCC CTG GAG GTG GAG GTG GGG ATA GGG GAG GAC H CAT L S A K E G I D G R G G G H H CTC TCC GCC AAG GAG GGC ATT GAT GGC CGC GGC GGA GGC GGG CAT CAT

H H * CAT CAT TAA

Figure 17GGG

Pfu DNA Polymerase (WT) -Sso7d fusion protein [Fig.17-GGG]

Nucleotide sequence (SEQ ID NO: 61) // Nucleotide sequence (SEQ ID NO: 71)

ccctggtcct gggtccacat atatgttctt actcgccttt atgaagaatc ccccagtcgc

tctaacctgg gttatagtga caaatcttcc tccaccaccg cccaagaagg ttatttctat

caactctaca cctcccctat tttctctctt atgagatttt taagtatagt tatagagaag

gttttatact ccaaactgag ttagtagata tgtggggagc ataatgattt tagatgtgga

ttacataact gaagaaggaa aacctgttat taggctattc aaaaaagaga acggaaaatt taagatagag catgatagaa cttttagacc atacatttac gctcttctca gggatgattc aaagattgaa gaagttaaga aaataacggg ggaaaggcat ggaaagattg tgagaattgt tttggaacat ccccaagatg ttcccactat tagagaaaaa gttagagaac atccagcagt aataccaatg gaggggaag aagagctaaa gattcttgcc ttcgatatag aaaccctcta tcacgaagga gaagagtttg gaaaaggccc aattataatg attagttatg cagatgaaaa tgaagcaaag gtgattactt ggaaaaacat agatcttcca tacgttgagg ttgtatcaag cgagagagag atgataaaga gatttctcag gattatcagg gagaaggatc ctgacattat tgggattaaa ttaaccattg gaagagatgg aagcgagccc aagatgcaga gaataggcga tatgacggct gtagaagtca agggaagaat acatttcgac ttgtatcatg taataacaag aaaggagaag gtatacgccg acgagatagc aaaagcctgg gaaagtggag agaaccttga cettecaatg gaaatteage ttteaagatt agttggacaa eetttatggg atgttteaag gtcaagcaca gggaaccttg tagagtggtt cttacttagg aaagcctacg aaagaaacga agtagctcca aacaagccaa gtgaagagga gtatcaaaga aggctcaggg agagctacac aggtggattc gttaaagagc cagaaaaggg gttgtgggaa aacatagtat acctagattt tagagocota tatocotoga ttataattao coacaatgtt totocogata ototaaatot tgatgtagag aaggttgaga aaaagtttct cggcaagcct attaccgtgt ggaaacttta tgtggacatc ttcgaatacg atattccatt tgcaaagaga tacctcatcg acaaaggcct agttacttat aatggagact cattcgactt cccatattta gcgaaaaggg cagaaaact gacaataaat ctcccaacat acacactaga ggctgtatat gaagcaattt ttggaaagcc gagagttgcc aaatactcga tggaagatgc aaaggcaact tatgaactcg ggaaagaatt Marked-Up Version

actagctgct aaaggagtta aaataaagcc aggaatggta attggataca tagtacttag tgagggatgc aagaactatg atatcgctcc tcaagtaggc cacaagttct gcaaggacat ccctggtttt ataccaagtc tcttgggaca tttgttagag gaaagacaaa agattaagac aaaaatgaag gaaactcaag atcctataga aaaaatactc cttgactata gacaaaaagc gataaaactc ttagcaaatt ctttctacgg atattatggc tatgcaaaag caagatggta ctgtaaaggag tgtgctgaga gcgttactgc ctggggaaga aagtacatcg agttagtatg gaaggagctc gaagaaaagt ttggatttaa agtcctctac attgacactg atggtctcta tgcaactatc ccaggaggag aaagtgagga aataaagaaa aaggctctag aatttgtaaa atacataaat tcaaagctcc ctggactgct agagcttgaa tatgaagggt tttataagag gggattcttc gttacgaaga agaggtatgc agtaatagat gaagaaggaa aagtcattac togtggttta gagatagtta ggagagattg gagtgaaatt gcaaaagaaa ctcaagctag agttttggag acaatactaa aacacggaga tgttgaagaa gctgtgagaa tagtaaaaga agtaatacaa aagcttgcca attatgaaat tccaccagag aagctcgcaa tatatgagca gataacaaga ccattacatg agtataaggc gataggtcct cacgtagctg ttgcaaagaa aggogatggt ccaattagca atagggcaat tctagctgag gaatacgatc ccaaaaagca caagtatgac gcagaatatt acattgagaa ccaggttctt ccagcggtac ttaggatatt aacttcctgg cttaacatta aaaaatccta gaaaagcgat agatatcaac ttttattctt tctaaccttt ttctatgaaa gaagaactga gcaggaatta ccagttcttc cgttatttta tgggtaatta aaaacccatg ctcttgggag aatcttcgaa taaaatccct aacttcaggc

gtagaagcgg cactactcag atgetteece aggaatgagg ttgttgtage tenteeenga tttgctaagt gaatagaata aacaacatca ctcacttcaa acgccttcgt tagaaatggt ctatctgcat gcttctctgg ctcggaanng gaggattcat aacaacagta tcaacattct cagagaattg agaaacatca gaaactttga cttctacaac atttctaact ttgcaactct tcaagatttt ctaaaagaat tttaacggcc tcctcgtcaa tttcgacgac gtagatcttt tttgctccaa gcagagccgc tccaatggat aacaccctg ttcccgcacc caagtccgct acaatttttt ccttgtatct cctaatgtat aagcaagcca aaggagagta gatgctacct ttccgggagt tttgtattgc tctagccaag gtttgggatt tttgaatcct ttaactctgg aaagtataat ttcaagctcc ttcttcttca tgacagatga aaaattgttt tgtctctttt taacttttac agaaataact gtctcaaatt atgacaactc ttgacatttt tacttcatta ccagggtaat gtttttaagt atgaaatttt tctttcatag aggaggnnnn nngtcctctc ctcgatttcc ttggttgtgc tccatatgat aagcttccaa agtgggtgtt cagactttta gacactcaaa taccagacga caatggtgtg ctcactcaag ccccatatgg gttgagaaaa aagattgaga tgttcttgg // // GCA ACC GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG // TGA CTG CAG ATG CTG GAG AAG CAG AAA AAG

Figure 17HHH

PPU DNA POLYMERASE (V93 R OR E)-Sso7d fusion protein [Fig.17-HHH]

Nucleotide sequence (SEQ ID NO: 27) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 28) // Nucleotide sequence (SEQ ID NO: 71)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 1320 1380 1500 1020 1080 1140 1200 1260 1440 1680 780 960 840 900 GGGAAGAAAG CAAGCCTATT TATAATGATT GGCAACTTAT TCAAAGAAGG AGTAGGCCAC CCTCTACATT GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG TCTTCCATAC ATATTTAGCG TGTATATGAA TGGACAACCT ACTTAGGAAA CAATGTTTCT GTTAGAGGAA AATACTCCTT CTGTTATTAG GCTATTCAAA CATTTACGCT TAACGGGGGA AAGGCATGGA TCTTGCCTTC CGAGCCCAAG TTTCGACTTG AGCCTGGGAA GTGGGAAAAC **LTATGGCTAT** AGAAAAGTT AAAGAGATAC TATCAGGGAG GLUTAMIC ACID) TTAGACCATA AAAACATAGA AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA AGTTTCTCGG CCACTATTAG TTCCATTTGC AGCTAAAGAT AAGGCCCAAT TTCTCAGGAT GAAGAATACA CACTAGAGGC AGATAGCAAA AAGATGCAAA CAAGATTAGT AAGCACAGGG AACCTTGTAG AGTGGTTCTT AAAAGGGGTT CTATAGAAAA TCTACGGATA GAAAAGTTTG GATTTAAAGT TCGCATTCCC GAGATGGAAG TAATTACCCA TCGCTCCTCA CCAAGTCTCT TGGGACATTT TTACTGCCTG V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR CGAAGGAGAA GAGTTTGGAA TACGCCGACG TACTCGATGG AAAGAGCCAG GCTGAGAGCG GATTGAAGAA GTTAAGAAAA GTTGAGAAAA GGGGAAGAAG GAAGGAAAAC GAATACGATA GGAGACTCAT GAAGTCAAGG ATTCAGCTTT AACTATGATA CAAGATXXXC ATTACTTGGA ATAAAGAGAT ACCATTGGAA CCAACATACA CCCTCGATTA ACTCAAGATC GCAAATTCTT V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, GATAGAACTT GATAGAGCAT GAGAGAGATG GGGATGCAAG AATGAAGGAA TGTAGAGAAG AGCAAAGGTG GACGGCTGTA GGAGAAGGTA AGTTGCCAAA TCCAATGGAA AGCCCTATAT TGGTTTTATA TAAGGAGTGT GGAGCTCGAA ATGATTTTAG ATGTGGATTA CATAACTGAA ACCAATGGAG TACTTATAAT GATTAAATTA AATAAATCTC TGGATTCGTT AAAACTCTTA GGACATCTTC GGAACATCCC TTTCAAGGTC TAGATTTTAG TTAAGACAAA GAATTGTTGA AACTTTATTT CAGCAGTTGT AAGGCCTAAT TAACAAGGAC ACCTTGAGAG GAAACGAAGT GCTACACAGG AGGACATCCC AAAAAGCGAT GATGGTACTG TAGTATGGAA ATGATTCAAA TAGGCGATAT GAAAGCCAAA AAGAATTCCT GAAAATTTAA CCCTCTATCA ATGAAAATGA TATCAAGCGA ACATTATAGT AAAAACTTGG TAAATCTTGA ACCGTGTGGA **FACATCGAGT** CTTCTCAGGG AGACAAAAGA GACTATAGAC AAAGAGAACG AGTTATGCAG AAGGATCCTG TATCATGTAA TTATGGGATG CTCAGGGAGA CCCGATACTC AAGTTCTGCA GCAAAAGCAA AGAGAACATC CTCATCGACA GATATAGAAA ATGCAGAGAA AGTGGAGAGA GAACTCGGGA GCCTACGAAA ATAGTATACC AAGATTGTGA GTTGAGGTTG AAAAGGGCAG GCAATTTTTG

GGC CTG TAC GAC GAG GCG CCG AAG GAG GAC ATC TCC 1860 1920 1980 2040 2160 1800 2100 AATAGATGAA TGAAGAAGCT AGCTGAGGAA ATACCAAAAG GCTTGAATAT TGAAATTGCA ACCAGAGAAG AGGICCICAC AATGGTAATT GGTTCTTCCA GTA ACC AACAAGACCA TTACATGAGT ATAAGGCGAT ATAAGAGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT TGGTTTAGAG ATAGTTAGGA GAGATTGGAG AATACAAAAG CTTGCCAATT ATGAAATTCC CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG GTA AAG TTC AAG TAC AAA GGC GAA GAA AAA GAG GTG GGC AAG ATG ATC TCC TTC GGT GCG GTA AGC GAA AAG GAC TTTGGAGACA ATACTAAAAC ACGGAGATGT TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT GTATGACGCA GAATATTACA TGGAGAACCA CATAAATTCA AAGCTCCCTG GACTGCTAGA TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC 2328 TGA ATG CTG GAG AAG CAG AAA AAG CGT CGT ACC GGC AAA GTA TGG ATGAGCAGAT TAAAAGAAGT AAAAGCACAA TTGTAAAATA TCATTACTCG AAGCTAGAGT AAG CTCGCAATAT GAAGGAAAAG GGATACATAG ACAAGACAAG ATC AAG CTG CAG GCTCTAGAAT GAAGGGTTTT GTGAGAATAG TACGATCCCA // GCA ACC GGT GGC AAAGAAACTC GTAGCTGTTG GCGGTACTTA

Eigure 17III

PFU DNA POLYMERASE (G387P/V93R OR E)-Sso7d fusion protein ${ m [Fig.17-III]}$

Nucleotide sequence (SEQ ID NO: 29) // Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 30)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) 360 420 G387P Mutant (CCN is the codon for Proline where $N=C,\ G,\ A,$ or T)AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA AAAAGGGCAG AAAAACTTGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG TATAATGATT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG CTGTTATTAG GCTATTCAAA CAAGCCTATT AGAAAAGTT AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG GLUTAMIC ACID) TTCCATTTGC GAATIGITGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG ACCAATGGAG GGGGAAGAAG AGCTAAAGAT AAAACATAGA ATAAAGAGAT TTCTCAGGAT CCACTATTAG CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC GGACATCTTC GAATACGATA AGCAAAGGTG ATTACTTGGA CAAGATXXXC GAGAGAGATG GGAACATCCC ACATTATAGT CAGCAGTTGT AAGGCCTAAT AACTTTATTT CCCTCTATCA ATGAAAATGA TATCAAGCGA CTCATCGACA AGTTATGCAG AAGGATCCTG AAGATTGTGA ACCGTGTGGA AGAGAACATC GATATAGAAA GTTGAGGTTG

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                          TACGCCGACG
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                                                                                                                                                                                                                                                                                                                                                              SCGGTACTTA
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ggG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAG GAG GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CAG AAA AAG // GCA ACC GTA AAG TTC AAG CTG CAG ATG CTG GAG AAG GGT GGC AAG ACC GGC CGT

Figure 17JJJ

PFU DNA POLYMERASE (D141A/E143A/V93R OR E) -Sso7d fusion protein [Fig.17-]]]]

Nucleotide sequence (SEQ ID NO: 31) // Nucleotide sequence (SEQ ID NO: 71)

Nucleotide sequence (SEQ ID NO: 32) // Nucleotide sequence (SEQ ID NO: 71)

793R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GCTACACA [CC N] GTTGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200 G, A, or T) 1020 1320 1380 1440 1680 1800 1080 GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140 1740 TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260 1500 1560 960 840 900 420 9 GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC CATTIACGCT TACGCCGACG AGATAGCAAA AGCCTGGGAA TGGACAACCT ACTTAGGAAA GTTAGAGGAA AATACTCCTT TTATGGCTAT GCTTGAATAT AATAGATGAA ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA CAAGCCTATT AGAAAAGTT TICCALITIGC AAAGAGATAC TCTTGCCTTC TCTTCCATAC TATCAGGGAG TACTIATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG CGAGCCCAAG TTTCGACTTG CACTAGAGGC TGTATATGAA GGCAACTTAT GGGAAGAAAG CCTCTACATT AAAGAAAAG TGAAATTGCA TGAAGAAGCT ACCAGAGAAG TATAATGATT D141A/E143A Mutant (GCN is the codon for alanine where N = C, GLUTAMIC ACID) GGGGAAGAAG AGCTAAAGAT TTCTCAGGAT ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA CAAGATTAGT TITCAAGGIC AAGCACAGGG AACCITGIAG AGIGGIICII CTATAGAAAA GAGATTGGAG ATGAAATTCC TTAGACCATA GTTGAGAAA AGTTTCTCGG CCACTATTAG GAGTTTGGAA AAGGCCCAAT AGCAAAGGTG ATTACTTGGA AAAACATAGA GAGATGGAAG GAAGAATACA TGGGACATTT TCTACGGATA GCTGAGAGCG TTACTGCCTG GTGAGGAAAT GGTATGCAGT ACGGAGATGT GATTTAAAGT GACTGCTAGA GATTAAATTA ACCATTGGAA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GAAAATTTAA GATAGAGCAT GATAGAACTT GAATACGATA ATAAAGAGAT CCAACATACA AAGAATTCCT TCCAATGGAA ATTCAGCTTT TGGTTTTATA CCAAGTCTCT ACTCAAGATC CTTGCCAATT CAAGATXXXC GAAGTCAAGG GCAAATTCTT GAAAAGTTTG GGAGGAGAAA CATAAATTCA AAGCTCCCTG ATTCTTCGTT ACGAAGAAGA TGGTTTAGAG ATAGTTAGGA TITGGAGACA ATACTAAAAC GGACATCTTC AATGAAGGAA CGAAGGAGAA GAGAGAGATG GACGGCTGTA GGAGAAGGTA TAAGGAGTGT GGAGCTCGAA AACTATCCCA AATACAAAAG TGTAGAGAAG GGAACATCCC ACCAATGGAG AATAAATCTC AAAACTCTTA CTTCTCAGGG ATGATTCAAA GAATTGTTGA CAGCAGTTGT AAGGCCTAAT ATGAAAATGA ACATTATAGT AAAAACTTGG TAGGCGATAT TAACAAGGAC GAAAGCCAAA TAAATCTTGA AGGACATCCC TTAAGACAAA AAAAAGCGAT GATGGTACTG TAGTATGGAA GTCTCTATGC ATAAGAGGGG TCATTACTCG AAGCTAGAGT TAAAAGAAGT AACTTTATTT CCCTCTATCA TATCAAGCGA TTGTAAAATA STAGCTGTTG GAACTCGGGA ATAGTATACC CCCGATACTC AGACAAAAGA GACTATAGAC GCTCTAGAAT GAAGGAAAAG AAAGAAACTC AAAGAGAACG AGAGAACATC AGTTATGCAG AGTGGAGAGA GCCTACGAAA CTCAGGGAGA AAGTTCTGCA GCAAAAGCAA GAAGGGTTTT GTGAGAATAG CTCGCAATAT AAGATTGTGA ACCGTGTGGA CTCATCGACA GCNATAGCNA GTTGAGGTTG AAGGATCCTG AAAAGGGCAG ATGCAGAGAA TATCATGTAA GCAATTTTG TTATGGGATG TACATCGAGT GACACTGATG

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2280
                                        2220
                                      TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA
                                                                            GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG
                                                                                                                  ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCC //
                                                                              GGATATTGGA
                                                                              GCGGTACTTA
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GGC CIG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG // TGA CTG CAG ATG CTG GAG AAG CAG AAA AAG CGT CGT TTC AAG GGT GGC AAG ACC GGC GTA TGG GTA AAG ATC AAG AAA // GCA ACC

Figure 17KKK

KOD DNA POLYMERASE - Sso7d fusion protein [Fig.17-KKK]

// Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 33) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 34)

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CGT (ALL POSSIBLE CODONS FOR ARGININE)
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                V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
                                                                                  CGGTTAAGCG GGTTGAAAAG GTTCAGAAGA AGTTCCTCGG
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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,
                                ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC
                                                GCGAGTTTAA GATTGAGTAC GACCGGACTT
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             GAGACCTCCT
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              ACTICCCAGG AITITAICCCG AGCCIGCIIG
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                                            TACAGGCAGA
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GGC GCG CCG AAG GAG CTG GAA AAA GAG GTA GAC ATC TCC GTG GGC AAG ATG ATC TCC TTC ACC TAC GAG GAG GGT GCG GTA AGC GAA AAG GAC TAC AAA GGC GAA ATG CTG GAG AAG CAG AAA AAG // CGT TTC AAG AAG ACC GGC CGT AAA GTA TGG GTA AAG GGT GGC CAG ATC AAG // GCA ACC

Figure 17L.L.L

Sso7d - kod dna polymerase fusion protein [Fig.17-LLL]

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Nucleotide sequence (SEO ID NO: 71) // Nucleotide sequence (SEQ ID NO: 33)
                                                                                         Nucleotide_sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 34)
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V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG,

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AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG
                                                            TCC TTC ACC TAC GAC GAG GGC
                                                                               GCG GTA AGC GAA AAG GAC GCG CCG AAG
GAG (ALL CODONS FOR GLUTAMIC ACID)
                                                             GGC AAG ATG ATC
                                                                                  GGT
                                                             CGT GTG
                                                                                  GGC CGT
                                           TIC
                                                             TGG
 V93E MUTANT: XXX = GAA,
                                           //GCA ACC GTA AAG
                                                             ATC AAG AAA GTA
                                                                                  GGT GGC AAG ACC
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AAA AAG

CAG

GAG AAG

CTG CAG ATG CTG

CGT (ALL POSSIBLE CODONS FOR ARGININE)

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/ATGATCCTCG ACACTGACTA CATAACCGAG GATGGAAAGC CTGTCATAAG AATTTTCAAG 60
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             AAGGAAAACG GCGAGTTTAA GATTGAGTAC GACCGGACTT TTGAACCCTA CTTCTACGCC 120
                            CATTGAGGAA GTCAAGAAGA TAACCGCCGA GAGGCACGGG
                                           GAGACCAGIT
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                                                                                                                                                                                                                                                                                                       CCTGTACCCC
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                             ACGATTCTGC
                                          CGGTTAAGCG
                                                                        CAGCAGTTAT
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                                                          AACTCTACTT
                                                                                                                                                   ACGTTCTCAT
                                                                                                                                                                   AAAAGCTCGG
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                                            ACGGTTGTAA
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                                                                                                                     AGCTACGCCG
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                                                                                                       GACATTGAAA
                                                                                                                                     GTTGACGTCG
                                                                                                                                                                                  ATTCAGAGGA
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Figure 17MMM

Sso7d-Vent DNA POLYMERASE FUSION PROTEIN [Fig.17- MMM]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 36) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 35)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA,

TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG GAG AAG CAG AAA AAG ggG GTA AAG CTG CAG ATG CTG GGT GGC AAG ACC //GCA ACC

1140 1200 1080 480 540 600 840 900 AGAGTATAAA GGGCAAAATA AGGTTTGTGG TACTCACAAC ACACTGATTA CATAACAAAA GATGGCAAGC CTATAATCCG AATTTTTAAG TTCAGCCCTA TATATAGCT TTTGCCGTAT TGAGGCAGTT TGCCGCTATA TGCTAGGGCA GTATCTTTA TCCGATAGTA GAGACATGGA AAGGGAAGTT CAAGCGTTAT CCTTGCCTTT AATAATGATT TGTTAAAGAA GTATCTCATA ACATCCCGAA AATCCACTTT GCTGATAGGT ACGATGTTGC TGCAGTGAAA GTCAGGAAAA AATTTTGGG CAGCTATGCG AGGGCGAGAT AAAATATCGA TTGTTCAAGT GGGACAAAGA TCAAGGGTAG CGTATACGCT CAGAGGAAAT CAATGGAAGA AGCTGGCAAA TCGTGGAGTG CTGATGAGGA AGCCAGAAAA CAATAATAGT TAAAGGGCGA TGACATTTAC GAATATGACA TACCCTTTGC GGAGACGAGG AGCTTAAGCT TTGATTTGCC TGTAAGAATT GAATTTGGAA GGCCAGAGTA ATCACATGGA CCGAACAAAC GGGAGTTTAA AATAGAACTT GACCCTCATT ATGGAAGCTG ACCGGCAACC TATGTAAAAG CTGTACCCTT TATTGAGGAG ATAAAGGCAA CGAGCATCCC CAAGACXXXC GTCTTAGGAA AAGGACGATA AACCTCCCAA AAATTAGGAG GCCCAGTACT ATAAAGCGTT GGGGACAATT GCTGTGGAAA TGAGGGAGAT AACCAAAAGC GAAAAAACTA STATCCCCAG ATACCCTTGA AAAAGAGGGC TCCCATGGAG AAGAGAAATG ATTCTTCCCC GAGATCAAGC CCTGGGAGGA TTTCCGCAGT AACTTACAAT AGTTCGGCTT TGATAGTTTT TGAACTTGCA CAGTTGTGCG TTTATTTGGA AGCTCATTTT CAGCTGTGGT AAAAGCTGGG AGAGGATGGG TCGGGAAGGA ATGACTCCGC GAGTGCTCGA AGGGCTTGAT CGTTTTATCA ATGTGATAAT TTTAGGAAA GGGACGTCTC ACGCGAGGAA GAACAACTTA ATGAAGAAGA TGTCCAATGA AAGAAAGCAT AGGGTGGCAT GAAAATATCA TATGAAGCAG TGGGAAACAG CAAAGTGTAT ATGATACTGG AAAGAGAACG CTTCTCAAAG AGTTATGCCG AAAGACCCCG AAACGGGCAG ACGTATGAGC CGGCGCTTAA GAAGTCTGGA AGGGAACATC CTCATAGACA GATATTGAAA CCCAAGATTC GATCTTTTCC AAAACTGTGA GTCGATGTTG

1800 1920 1980 2100 2160 1560 1620 1680 1740 1860 2040 2220 1440 GGACTTAATT CGAAAAGAAA CGGCTATATG TAAGGTTCTT ACTCATTAAA GCTTGAGCTT TGCAGTCATA TTGGAGTGAG AAGTGTTGAA GGTTCCACTT AGCCATTGGC ACCGGGCACA AAACCAAGTT TTTAAGGTAT CGCATGGGGG AATTTACTT TTAAAGAGGG AGGACTACAA ACAGCTATTA AAAAGCGCTA TAAAAGTGAA CCATACTCGG TTGACCCGAT AGTTCGGCTT AAAAGCCTGA TTCCAGGTCT TAAGGAGAGA CAAAATACAG GCGATAGGGT ACTACATAGA GAAAGGAGGA AAAGCGTTAC GGTAG 2325 TTTGTTACAA TTTATTCCCT GAAGAAATG AAATCCACAA TTGCTTGCAA GAATGTGCTG ATAGAGGAAA ATACCCGGGG AACTCCAAAC TTGGAAGTAG GAGGCTATAC GAGAAAATAG AGGGATTTAA GCAAGAGGGA GGAAAGATAA GATCCGGACT TTTGGATACA CAAAGCTCAA AACAAACCGG CTTAGATGCA TGGCTCAAGA CTTTCCGGGC AAACTACATA ACTCGAAGCG GGCTATTAAA GATAAGAGAA GAGAGGATTC GCAGATTACC AAGACTTGCC GTACTCGAAG TTATGCCACA AACAAGGGGC AAAGGTTTTA AGATGTTGTA CAAAGGGAGC ACACAAGTAC TCTGCAAGGA AGGAATTCCT AAGTTGTTAG CGATAGCAAA TACTTAGGAT AAGATATAAA ATAGGCAAAG AGGCAAGATG TAGAGATGAC CTGACGGCTT GCTTTTACTT GCAGGATAAC AGACTCAGGC TTATCCATGA ATATCGTTCT ATCCTAGAAA GCAATGAGGC ACAGAATACG GGATATAGGT AAGAAAGCCA GAGTATGAGG ATAGCTAAGG AAAGCTGTAG CCTCATGTCG ATAATAAGCT TTGCCGGCAG ATGCTCGATT GGGTATCCTA AGACACTACA TATGCGGACA GATGAAGAGG GAAAAGCTTG

Figure 17NNN

Vent DNA POLYMERASE - Sso7d FUSION PROTEIN [Fig.17-NNN]

// Nucleotide sequence (SEQ ID NO: 71) Nucleotide_sequence (SEQ ID NO: 36) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 35)

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793R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
                                                                              V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
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300
                                                                         360
                                                                                                                     540
                                                                                                                                   900
                            GAGACATGGA
                                           AAGGGAAGTT
                                                          GGGCAAAATA
                                                                        CAAGCGTTAT
                                                                                                                     TTTGCCGTAT
                                                                                                                                   TGTTAAAGAA
                                                                                                                                                  GTATCTCATA
                                                                                                                                                                ACATCCCGAA
CTATAATCCG AATTTTAAG
                                                                                                       AATAATGATT
               TATATATGCT
                                                                                       CCTTGCCTTT
                                           AATTTTGGG
                                                        CAGCTATGCG
                                                                                                                                                                GGGACAAAGA
             TTCAGCCCTA
                                                                                                                                                 TIGATITGCC
                             TAAAGGGCGA
                                                                        TACCCTTTGC
                                                                                       AGCTTAAGCT
                                                                                                       AGGCCGAGAT
                                                                                                                     AAAATATCGA
                                                                                                                                   TIGITICAAGT
                                           GTCAGGAAAA
                                                                                                                                                                GTCTTAGGAA
ATGATACTGG ACACTGATTA CATAACAAAA GATGGCAAGC
             GACCCTCATT
                            ATAAAGGCAA
                                                         CAAGACXXXC
                                                                        GAATATGACA
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                                                                                                       GAATTTGGAA
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                                                                                                                                                  GGGGACAATT
                            TATTGAGGAG
             AATAGAACTT
                                                         CGAGCATCCC
                                                                          TGACATTTAC
                                                                                       TCCCATGGAG
                                                                                                      TGAGGGAGAT
                                                                                                                     GGCCAGAGTA
                                                                                                                                   AAGAGAAATG
                                                                                                                                                                AAACGGGCAG AAAAGCTGGG AGTTCGGCTT
                                            TGCAGTGAAA
                                                                                                                                                   AACTTACAAT
              GGGAGTTTAA
                            ATGACTCCGC
                                                                                                                                                  AAAGACCCCG ATGTGATAAT
                                            GAGTGCTCGA
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                                                                         CAGCTGTGGT
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                                                                                                        CGTTTTATCA
                                                                                                                     ATGAAGAAGA
                                                                                                                                   TGTCCAATGA
                            CTTCTCAAAG
                                           AAAACTGTGA
                                                                                       CTCATAGACA
                                                                                                                    AGTTATGCCG
                                                                                                                                   GTCGATGTTG
               AAAGAGAACG
                                                          GAAGTCTGGA
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                                       960
                          TGCCGCTATA
                                      TGCTAGGGCA
                                                   GCTGATAGGT
                                                                 GTATCTTTA
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                                                                                                          TACTCACAAC
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AATCCACTTT
             TGAGGCAGTT
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TCAAGGGTAG
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             CGTATACGCT
                                       CAATGGAAGA
                                                    AGCTGGCAAA
                                                                 TCGTGGAGTG
                                                                                            AGCCAGAAAA
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                                                                                                                                                 TTGACCCGAT
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                                                                                                                                                                           AAAGCGTTAC
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                                                                                                                                                                                                                                                                                                                                                       CTTAGATGCA TGGCTCAAGA GG 2325 //
            CAGTIGIGG AAGGACGATA AACCICCCAA
                                                                                                                                                            TTGCTTGCAA
                                                                                                                                                                                                      ATACCCGGGG
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GCTGTGGAAA
                          AACCAAAAGC AAATTAGGAG
                                       GCCCAGTACT
                                                    ATGGAAGCTG
                                                                 ACCGGCAACC
                                                                               CCGAACAAAC
                                                                                            TATGTAAAAG
                                                                                                          CTGTACCCTT
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                                                                                                                                    TTTATTCCCT
                                                                                                                                               GAAGAAATG AAATCCACAA
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TGATAGTTTT
                                                    ATTCTTCCC
                                                                GAGATCAAGC
                                                                                                                     AAAAGAGGC
                                                                                                                                  CTTTCCGGGC
                                                                                                                                                             GGCTATTAAA
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                                       GAAAAACTA
                                                                              TGAACTTGCA
                                                                                            CCTGGGAGGA
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                                                    TCGGGAAGGA
                                                                              ACGCGAGGAA
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                                                                                                                                                                                        TAGAGATGAC
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AGAGGATGGG
                           TTTTAGGAAA
                                       AAGAAAGCAT
                                                                 GGGACGTCTC
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                                                                                                          TTTATTGGA
                                                                                                                       ATACCCTTGA
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                                                                                                                                                             ATAGGCAAAG
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CCCAAGATTC
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                                                                                                                                  GGATATAGGT
                                                                                                                                                GCAATGAGGC
                                                                                                                                                                                                                    AAGAAAGCCA
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             GATCTTTCC
                          TATGAAGCAG
                                       TGGGAAACAG
                                                    ACGTATGAGC
                                                                 CAAAGTGTAT
                                                                               AGGGTGGCAT
                                                                                            CGGCGCTTAA
                                                                                                          GAAAATATCA
                                                                                                                                                              ATGCTCGATT
                                                                                                                                                                            GGGTATCCTA
                                                                                                                                                                                        AGACACTACA
                                                                                                                                                                                                       TATGCGGACA
                                                                                                                                                                                                                                GAGTATGAGG
                                                                                                                                                                                                                                              GATGAAGAGG
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                                                                                                                                                                                                                                                                                                  CCTCATGTCG
                                                                                                                                                                                                                                                                                                                ATAATAAGCT
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AAG
        GGG
               CTG
GAC ATC TCC
       TAC GAC GAG
               GAG
               CCG AAG
       TTC ACC
               gcg
 GTA
               GAA AAG GAC
 GAA AAA GAG
       ATC TCC
                       TGA
       GGC AAG ATG
 AAA GGC GAA
              GCG GTA AGC
                       AAA AAG //
TAC
                       CAG
        GTG
               GGT
AAG
        CGT
               CGT
                       AAG
                       GAG
AAG TTC
               ACC GGC
        GTA TGG
 GTA
         AAA
               GGC AAG
                       ATG
                       CAG
        ATC AAG
GCA ACC
               GGT
=
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Figure 17000

Deep Vent- Ssod7 DNA polymerase fusion protein $[{ m Fig.17-000}]$

Nucleotide sequence (SEQ ID NO: 38) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 37) // Nucleotide sequence (SEQ ID NO: 71)

CGT (ALL POSSIBLE CODONS FOR ARGININE) 420 480 540 600 99 720 780 840 900 960 1020 1140 1200 1260 1320 1500 1560 240 300 360 1080 1380 1440 1620 1680 1740 1800 GAGGCATGGG GCTTGAGTAC GATAGATGAG CGAAATAGCC CGATTATAAG GATTTTCAAG GGATAAGATA GAAGAGGTAC TATAATGATA GATAAGGGAG GGCCTGGGAG CGAGAGAAGG TAACGICICA GAAGATGCTT TTATGGGTAC GGGGAGGGAA CTTATACATA AAAGAAGAAA CATTTACGCT GAGGCCGATT GCTCGCATTT TCTCCCGTAC TGAGCCAAAG CTTTGACCTC AGTTTATGAG GGTAACGTAC CGGCCAGCCC CCTCAGGAAG CTGGGAGGGG GGTTGGGCAC ATTGGATGAA CTATCTAGTT GLUTAMIC ACID) TTAGACCTTA CCGCAATAAG AGATAGCTGA TATTCAATGG AGGATGCAAA AGTGGTACCT TAATCACCCA TCAAGAGGTT ATTATGGGTA GGTTCAAAGT CCGAGGAGAT SAAGGGAAGA TAATCACTAG GGGGCTTGAA ATAGTCAGGA GGGACTGGAG TAACCGCCGA AGTTCCTGGG AGGGGCCCAT TCCTCAAGGT TCGACCTTCC GAAGGATACA CCCTCGAGGC AAGGAGCCGG AGAAAGGGCT TCGCCCCAGA CAATCGAGAA TTACGGCCTG GITCTICGIG ACGAAGAAGA AGIAIGCGII TTCCGTTCGC AGCTCAAGTT AAAAGATCGA GGGACGGTAG CAAGGTTAGT AAGCCGGATG AGAGGGAGTA GGCTGTTGGA V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GGCGATGAAG TACGCTCACG CCCAGCCTGC GGGCCAAAAC AAGCTCCCAG V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, ATGATACTTG ACCCTGACTA CATCACCGAG GATGGGAAGC GTTAGGAAGA GAGTTCGCGA AACTTGGTGG GAATACGATG TCTAAAGACC GCAGAGAGCG GAAAAGTTCG GACAGAAACT GTAAGGAAGA CAGGACXXXC GAGTACGACA ATAACGTGGA ATAAAGCGGT GGCGATTCTT CCCCTGGGAA GAGATAAAGG CCAACATACA GCCCAGCTTT CCCTCGATAA GCAAACAGCT TATAAACGCC AGTTGCAAAG GGCTCCAAAC GGGATACGTT CACAATTCCT GATTGATGAG GGCTGTACTT TGAACACCCT GAGGGAGATG TACCTACAAC TTCAACTGGC GAGCCTGTAC GGGGTTTATC GATGAAAGCT TAAGGAGTGC GGAACTGGAG AAAGAAACG GCGAGTTTAA GGTTGAGTAC TGCCGAAAAG TGACATCTTT TCCAATGGAA CGAAGGGGAG GATAAAGCTA GACAGCGGTG GGAGAAAGTT CCCAATGGAG AGGGTGTAGG CAAAATCCTG AGCCAAAGTC GATAAACCTC GAGGGCTTCT ACGTGAGAGG CTCCTCAAAG ATGACTCGCA CCGCAGTTAT GACTGGAGAG GCTACGCTGG TAGATTTCAG TGAACAGGGA AGGACTTCCC AACGGGCAAT GTTGGTACTG TCGTAAGGAA GACTCTACGC TCGTAGATTA GAATTATAGA AAGGCCTAAT CCCTCTATCA ATGAGGAAGA TTTCCAGCGA ATGTTATAT AAAAGCTCGG TTGGGGATAT TTAGGAGAAC GAAAGCCAAA GGGAGTTCTT TTTCTAGGTC GGAATGAATT TAAAAAGGAA GATTACAGGC GCCCTAGAGT GCAATCTTCG CTGTGGGATG CTAAGGGAGA TTAGTTTCCC GACACAGATG AAGATAGTGA GAGGTATGGA GTCGAGGTAG AAGAGGGCCG TACCACGTGA ACTGGAAAGG GAGCTCGGTA GCCTACGAGA CCGGATACGC AAGTTCTGCA AGGCAAGAAA GCAAAAGCCC TATATAGAGT AGAGAGCATT CTAATAGACA GACATAGAAA AGCTATGCTG AAAGATCCCG ATGCAGAGGC

1980 2040 2100 2160 2220 2280 1920 GGCCTTTGGG TACAGGAAAG AAGACCTCAG GTGGCAGAAG TGAGGAGGCA TTAAGGAGGT AACTGAAAAG CTGAGCAAGT ACGAAATACC TCCAGAAAAG AGGTCCGCAC CATGGTGATA TGCAGAGGAG GGTTTTACCT CTTCACGAGT ACAAGGCTAT AGACGGCCA ATAAGCAAGA GGGCTATCCT GTATGACGCT GAGTATTACA TAGAAAATCA CCTAGAGGCT ATCCTAAAGC ATGGCAACGT TGAGGCCTGG GGCATGGCTT AACATCAAGA AGAAG GGAGTAAAGG CACGAGGCCC AGCCGCTAGA TGCTGAGGGG CAGGTCTTAC AAGCAAAAGT ACGAGCAGAT CAAAAAGGTT GAATATTAGA GGAAGCATAA GTAAAGATAG AAAGAAACCC ACTAAACAGA CTAGTTATTT GGGTACATAG GCCGTTCTTA GTTGCCGTGG TTCGATCTCA

GGG GAA AAG GAC GCG CCG AAG GAG CTG GAA AAA GAG GTA GAC ATC TCC AAG GTG GGC AAG ATG ATC TCC TTC ACC TAC GAG GAG AAG ACC GGC CGT GGT GCG GTA AGC ATG CTG GAG AAG CAG AAA AAG // TAC AAA GGC GAA CGT TTC AAG AAA GTA TGG GGT GGC AAG ACC GGC GTA AAG ATC AAG CTG CAG // GCA ACC

Figure 17PPP

Ssod7 - Deep Vent DNA polymerase fusion protein [Fig.17-PPP]

// Nucleotide sequence (SEQ ID NO: 38) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 37) Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) GAG (ALL CODONS FOR GLUTAMIC ACID) V93E MUTANT: XXX = GAA,

TIC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC AIC ICC AAG TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG GAG AAG CAG AAA AAG CGT GGT ggc //GCA ACC GTA AAG ATC AAG AAA GTA GGC AAG ACC CTG CAG ATG CTG GGT

120 180 240 300 GATTTTCAAG CATTTACGCT GAGGCATGGG GAGGCCGATT GAGGTATGGA GGCTGTACTT TGAACACCCT CAGGACXXXC CCGCAATAAG GGATAAGATA ACGCTGACTA CATCACCGAG GATGGGAAGC CGATTATAAG ATGACTCGCA GATTGATGAG GTTAGGAAGA TAACCGCCGA TGCCGAAAAG GTAAGGAAGA AGTTCCTGGG TTAGACCTTA GCGAGTTTAA GGTTGAGTAC GACAGAAACT GAATTATAGA AAAGAAAACG CTCCTCAAAG AAGATAGTGA ATGATACTTG

360	480	540	009	099	720	780	840	900	960	1020	1080	1140	1200	1260	1320	1380	1440	1500	1560		1680	1740	1800	1860	1920	1980	04		2160	2220	2280	2328
GAAGAGGTAC	TATAATGATA	TCTCCCGTAC	GATAAGGGAG	CTATCTAGTT	TGAGCCAAAG	CTTTGACCTC	AGTTTATGAG	GGCCTGGGAG	GGTAACGTAC	CGGCCAGCCC	CCTCAGGAAG	CGAGAGAAGG	CTGGGAGGGG	TAACGTCTCA	GGTTGGGCAC	ATTGGATGAA	GAAGATGCTT	TTATGGGTAC	GGGGAGGGAA	CTTATACATA	AAAGAAGAAA	GCTTGAGTAC	GATAGATGAG	CGAAATAGCC	TGAGGAGGCA	TCCAGAAAAG	AGGTCCGCAC	CATGGTGATA	TGCAGAGGAG	GGTTTTACCT	GTGGCAGAAG	
TTCCGTTCGC	AGGGGCCCAT	AAAAGATCGA	TCCTCAAGGT	TCGACCTTCC	GGGACGGTAG	GAAGGATACA	CCCTCGAGGC	AGATAGCTGA	AGGATGCAAA	CAAGGTTAGT	AGTGGTACCT	AGAGGGAGTA	AGAAAGGGCT	TAATCACCCA	TCGCCCCAGA	TCAAGAGGTT	CAATCGAGAA	ATTATGGGTA	TTACGGCCTG	GGTTCAAAGT	CCGAGGAGAT	GGCTGTTGGA	AGTATGCGTT	GGGACTGGAG	ATGGCAACGT	ACGAAATACC	ACAAGGCTAT	TGAGGCCTGG	GGGCTATCCT	TAGAAAATCA	AAGACCTCAG	AGAAG TAA
GAGTACGACA	GAGTTCGCGA	ATAACGTGGA	ATAAAGCGGT	GGCGATTCTT	CCCCTGGGAA	GAGATAAAGG	CCAACATACA	TACGCTCACG	TATTCAATGG	GCCCAGCTTT	AACTTGGTGG	AAGCCGGATG	AAGGAGCCGG	CCCTCGATAA	GAATACGATG	CCCAGCCTGC	TCTAAAGACC	GCAAACAGCT	GCAGAGAGCG	GAAAAGTTCG	GGGCCAAAAC	AAGCTCCCAG	ACGAAGAAGA	ATAGTCAGGA	ATCCTAAAGC	CTGAGCAAGT	CTTCACGAGT	GGAGTAAAGG	ATAAGCAAGA	GAGTATTACA	TACAGGAAAG	AACATCAAGA
TGACATCTTT	CGAAGGGGAG	AGCCAAAGTC	GAGGGAGATG	TACCTACAAC	GATAAAGCTA	GACAGCGGTG	GATAAACCTC	GGAGAAAGTT	AGTTGCAAAG	CCCAATGGAG	TTCAACTGGC	GGCTCCAAAC	GGGATACGTT	GAGCCTGTAC	AGGGTGTAGG	GGGGTTTATC	GATGAAAGCT	CAAAATCCTG	TAAGGAGTGC	GGAACTGGAG	CACAATTCCT	TATAAACGCC	GTTCTTCGTG	GGGGCTTGAA	CCTAGAGGCT	AACTGAAAAG	CACGAGGCCC	AGCCGCTAGA	AGACGGGCCA	GTATGACGCT	GGCCTTTGGG	GGCATGGCTT
CCGCAGTTAT	CCCTCTATCA	ATGAGGAAGA	TTTCCAGCGA	ATGTTATAAT	AAAAGCTCGG	TTGGGGATAT	TTAGGAGAAC	GAAAGCCAAA	GACTGGAGAG	GGGAGTTCTT	TTTCTAGGTC	GGAATGAATT	GCTACGCTGG	TAGATTTCAG	TGAACAGGGA	AGGACTTCCC	TAAAAAGGAA	AACGGGCAAT	GTTGGTACTG	TCGTAAGGAA	GACTCTACGC	TCGTAGATTA	ACGTGAGAGG	TAATCACTAG	AAGCAAAAGT	TTAAGGAGGT	ACGAGCAGAT	CAAAAAGGTT	TGCTGAGGGG	GGAAGCATAA	GAATATTAGA	CAGGTCTTAC
AGAGAGCATT CTAATAGACA	GACATAGAAA	AGCTATGCTG	GTCGAGGTAG	AAAGATCCCG	AAGAGGGCCG	ATGCAGAGGC	TACCACGTGA	GCAATCTTCG	ACTGGAAAGG	GAGCTCGGTA	CTGTGGGATG	GCCTACGAGA	CTAAGGGAGA	TTAGTTTCCC	CCGGATACGC	AAGTTCTGCA	AGGCAAGAAA	GATTACAGGC	GCAAAAGCCC	TATATAGAGT	GACACAGATG	GCCCTAGAGT	GAGGCCTTCT	GAAGGGAAGA	AAAGAAACCC	GTAAAGATAG	CTAGTTATTT	GTTGCCGTGG	GGGTACATAG	TTCGATCTCA	GCCGTTCTTA	ACTAAACAGA

Figure 17000

JDF-3 - Sso7d fusion protein $ilde{ t Fig.17-QQQ}$

Nucleotide_sequence (SEQ ID NO: 40) // Nucleotide sequence (SEQ ID NO: 71) Nucleotide sequence (SEQ ID NO: 39) // Nucleotide sequence (SEQ ID NO: 71)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAGGAGTTAAACTCATGTCCTTCGACATCGAGACGCTCTACCACGAGGGGAGAAGAGTTTGGAA ACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCAAAAAGATAACCGCGGAGGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAGTTCCTCGG CAGGICTGIGGAGGICTGGGICCTCTACTICACGCACCCGCAGGACXXXCCGGCAAICCGCGACAAAATAAGGAAGCACCCCGCGGGTCAICGACAICTACGAGIACGACATACCC ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGCTTTGAGAG ACGCCGGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACATATCGTGTATCTAGACTTTCGTAGTCTTCTACCTTCAATCATCATACCCCACAACGTCTCGCCAGATAC CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGGGGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT GAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGC GITAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGTTCGACCCGACGAAGCACAAGTACGATG GCGCTTCTTGAGGGTCGTTAAGGAAAGGACCCCGGACGTGCTGATAACATACAACGGCGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTTGGCGTGA ACCCTCGGGAGGGACGGGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACATAA **GGTCGCGCCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC** ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGGTGGTTGGGGAAAAGTTCGGTTTTAAAGTCCT ACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAAA CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCCGC TGATCCTTGACGTTGATTACATCACCGGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAGGAGGTGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCTTACTTTCT CTATGCAGACACAGACGGTCTCCATGCCACCATTCCTGGAGCGGCGGTCGAAACAGACAAAAAAGGCAATGGAGTTCTTAAACTATATCAATCCCAAACTGCCCGGCCTTCTC GTGGCTGAAGCCGAAGGGGAAGAAGAAG//

TTC AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC GGC CGT GCT GCG GTA AGC GAA AAG GAC GCG AAG GAG CTG GAG AAG CAG AAA AAG CTG CAG ATG CTG //GCA ACC GTA AAG ATC AAG AAA GTA GGT GGC AAG ACC

Figure 17RRR

Sso7d - JDF-3 fusion protein [Fig.17-RRR]

Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 40) Nucleotide sequence (SEQ ID NO: 71) // Nucleotide sequence (SEQ ID NO: 39)

V93R MUTANT: XXX = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE) V93E MUTANT: XXX = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

GGT GGC AAG ACC GGC CGT GGT GCG GTA AGC GAA AAG GAC GCG CCG AAG GAG CTG CTG CAG AAG CAG AAA AAG $^{\prime\prime}$ AAG TAC AAA GGC GAA GAA AAA GAG GTA GAC ATC TCC AAG ATC AAG AAA GTA TGG CGT GTG GGC AAG ATG ATC TCC TTC ACC TAC GAC GAG GGC //GCA ACC GTA AAG TTC

TTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGATGGAAGGTGAGGAAGAGCTTAAACTCATGTCCTTQGAQATQGAGACGTCTACCACGAGGGAGAAGAGTTTGGAA acgecegtegetaceteaaggagecegaagegggactgtgggacaatatcgtgtatetagaettttcgtagtetetad<mark>eet</mark>fcaatcataatcacecacaacgtetegecagatae CAGAAGATAAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGTCTCCTCGATTACAGGCAACGGCGATCAAGATTCTCGCCAACAGCTACTACGGCTACTACGGCT CAGGTCTGTGGAGGTCTTGGGTCTTCACGCACCCGCAGGACXXXCCGGCAATCCGCGACAAATAAGGAAGCACCCCGCGGTCATCGACATCTACGAGTACGACATACCC GCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGGACGTGCTGATAACATACGACGACAACTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGGCGTGAGCTTT ACCCTCGGGAGGGAGGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACACTTCGACCTTTATCCAGTCATAAGGCGCACATAA ACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTTTCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCCTGGGAGACCCGGCGAGGGGCCTTGAGAG GTCGCGCGCTACTCGATGGAGGGCGAGGGTTACCTACGAGGCTTGGCAGGGAGTTCTTCCCGGATGGAGGCCCAGCTTTCCAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCC ATGATCCTTGACGTTGATTACATCACCGGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAGAGGGCGAGTTCAGGATTGAATACGACCGCGAGTTCGAGCCCTACTTCT ATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTACGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTCGGTTTTAAAGTCCT A CTCGAATA CGAGGCTTCTACGTCAGGGGCTTCTTCGTCACGAAGAAAAGTACGCGGTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGC ACTGGAGCGAGATAGCGAAGGAGGCGAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAATTGTCAGGGAAGTCACCGAAAAGCTGAGCAA GTACGAGGTTCCGCCGGAGAAGCTGGTTATCCACGAGCAGATAACGCGCGAGCTCAAGGACTACAAGGCCACCGGCCCGCACGTAGCCATAGCGAAGcGTTTGGCCGCCAGAGGT STTAAAATCCGGCCCGGAACTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGAGGTTCGACCCGACGAGGAAGCAAGTACGATG CGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCCTCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGC GTGGCTGAAGCCGAAGGGGAAGAAGAGTGA

SEQ. ID. NOS.	73 74	75 76			7/7/8	82	86/87/88	16/06/68	92/93 94/95	86/16/96	99/100/101	102/103/104	101/109/100	108/109	111/112/113			
[F1g. 18]	valvydaefvgserefeeeretflk@vkpydgvlat@ylmegsssagnde@llelhq ggn2lkfyasvgldirgigaigdgwvg	vpin ekeerin eigrenpwtphdgigrig Ginsvoe gekdpessgiyslwsrvvn in ridrkin neigkdgRRiSnglik krousvst treerrr α α	\boldsymbol{q}	← — Motif 1 — — ♦	lkLqdrygiredvylcLaraFdgsismiattpyrtlkdvc pdltleeAksvnrtl atLidehGlspdaMdeLiehFeSiagila tdleeiErmyz eGrlseeAyraavei	LtkkeGVGrkt en LlrafgnperVkglarefei EkLasVeGvGervlrsl	rGidrerherlikkyGgyskv reagveelre dGltdaqirelkg vydlekydelkykygssav rrlnyskirs lafeddelaelka	kklreafdlethaebyerygslkeig rrlsyddilE lgatpkaAae	LinieGVGpklaelineavdydlerl aslnpEELaEVeGlGeelAervvy	ewierkydegraffinieyfdsageygkiyenaeyskui ypdigdeayari thrdagltpaeMervikryGSvskVq — egatpdEhrE 1GlGdakiari	sLvnkrldvdt yelkrryg Svsav rkapvk Elr E l Gladrkiar I	nLqvrGmsvekRerLLerFdtwtkV keapvsELv VpGvGlslvkelkaq	LidvkGvspel@driveelGSpyrv ltakksdim VervGpklAerIra	LiktnGVGpk1回1ailbgmbaqqfV naverEEvga1pGiGkktAerlive akklugvG+kiMemideflatoklrklekirnddtsssiveGiGnsalrkfvde	vmevpGVGpktArgLyealGidsle klkealergdLl lkGfGakkAerIke	gvg A 11 ygs u u eu eu gug u u		α β α α α β α
	MkTpV 1 RecA VI	MKTDV 179 HTH asnC HTH SS			A 299 B 354	41	46	56	62	7 5	80	82	91	ECRUVA 73	•	Consensus	HhH SS	

EIGURE 18 (cited from Belova et al. (2001) Proc. Natl. Acad. Sci 98: 6015-6020)

FIGURE 19 [Fig. 19]

SEQ ID NO: 120 Synthetic Sso7d gene

GCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGACATCTCCAA GATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTACGACGAGGG CGGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAGGACGCGCCGAAGGAGC TGCTGCAGATGCTGGAGAAG CAGAAAAAG

SEO ID NO: 121 The amino acid sequence of Sso7d.

 $ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQ\\ MLEKQKK$

SEQ ID NO: 122 The DNA sequence encoding the Sso7d-ΔTaq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAA GAGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCC TTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCT GGCCGCCGCCAGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAAGCCCT CAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGC CCTGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTAC CTCCTGGACCCTTCCAACACCACCCCGAGGGGGTGGCCCGGCGCTACGGCGGG GAGTGGACGGAGGGGGGGGGGGGGCCCCCTTTCCGAGAGGCTCTTCGCC AACCTGTGGGGGAGGCTTGAGGGGGGAGGAGGCTCCTTTGGCTTTACCGGGAG GTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGC CTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCC GCCTCGAGGCCGAGGTCTTCCGCCTGGCCGCCACCCCTTCAACCTCAACTCCCG GGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAA GACGGAGAAGACCGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCG CGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCT GAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGCCG CCTCCACACCGGCTTCAACCAGACGGCCACGGCCACGGCCAGGCTAAGTAGCTC CGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGC CGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAG ATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCT TCCAGGAGGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCC CCCGGGAGGCCGTGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCG GGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCCCTTA CGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGG GCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGAC CCTCTTCGGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGT GCGGGAGCGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGC CGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGG GGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGA GAGGGCGAGGCCGTGGCCGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCC CCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGGACTGGCTCTCCGC CAAGGAGGCATTGATGGCCGCGGCGGAGGCGGCATCATCATCATCATTA A

SEQ ID NO: 123 The amino acid sequence of Sso7d-ΔTaq fusion protein

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLQMLEKQKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAA ARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDP SNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERPLS AVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLF DELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIH PRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYS QIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGV LYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRR RYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLL QVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDGR GGGGHHHHHH

SEQ ID NO: 124 The DNA sequence encoding the Sso7d-Taq fusion protein

ATGATTACGAATTCGAGCGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAA GAGGTAGACATCTCCAAGATCAAGAAGTATGGCGTGTGGGCAAGATGATCTCC TTCACCTACGACGAGGGCGTGGCAAGACCGGCCGTGGTGCGGTAAGCGAAAAG GACGCGCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGGGCGGCGG TGTCACTAGTGGGATGCTGCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTG GACGCCACCACCTGCCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCA GCCGGGGGAGCCGTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGG CCCTCAAGGAGGACGGGGACGCGTGATCGTGGTCTTTGACGCCAAGGCCCCCT CCTTCCGCCACGAGGCCTACGGGGGGTACAAGGCGGGCCGGGCCCCACGCCAG AGGACTTTCCCCGGCAACTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCT GGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGACGTCCTGGCCAGCCTGGC CAAGAAGGCGGAAAAGGAGGCTACGAGGTCCGCATCCTCACCGCCGACAAAG ACCTTTACCAGCTCCTTTCCGACCGCATCCACCTCCACCCCGAGGGGTACCT CATCACCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGC CGACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGG CATCGGGGAGAAGACGCCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAG CCCTCCTCAAGAACCTGGACCGCCTGAAGCCCGCCATCCGGGAGAAGATCCTGG CCCACATGGACGATCTGAAGCTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCT GCCCTGGAGGTGGACTTCGCCAAAAGGCGGGAGCCCGACCGGGAGAGGCTTAG GGCCTTCTGGAGAGGCTTGAGTTTGGCAGCCTCCTCCACGAGTTCGGCCTTCTG GAAAGCCCCAAGGCcCTGGAGGAGGCCCCCTGGCCCCGCCGGAAGGGGCCTTC GTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGATCTTCTGGCCCTGG CCGCCGCAGGGGGGCCGGGTCCACCGGGCCCCGAGCCTTATAAAGCCCTCA GGGACCTGAAGGAGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCCC TGAGGGAAGGCCTTGGCCTCCGCCGGCGACGACCCCATGCTCCTCGCCTACCT CCTGGACCCTTCCAACACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGA GTGGACGGAGGAGGCGGGGGGGCCCCTTTCCGAGAGGCTCTTCGCCAA CCTGTGGGGAGGCTTGAGGGGGAGGAGGCTCCTTTGGCTTTACCGGGAGGT GGAGAGGCCCTTTCCGCTGTCCTGGCCCACATGGAGGCCACGGGGGTGCGCCT GGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGCCGAGGAGATCGCCCG CCTCGAGGCCGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCGG GACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTCCCGCCATCGGCAAG ACGGAGAAGACCGCCAGCGCTCCACCAGCGCCGCCGTCCTGGAGGCCCTCCGC GAGGCCCACCCATCGTGGAGAAGATCCTGCAGTACCGGGAGCTCACCAAGCTG AAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCC TCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCAGGCTAAGTAGCTCCG ATCCCAACCTCCAGA. ACATCCCCGTCCGCACCCCGCTTGGGCAGAGGATCCGCCG GGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGAT AGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTC CAGGAGGGGGGACATCCACACGGAGACCGCCAGCTGGATGTTCGGCGTCCCC

CGGGAGGCCGTGGACCCCTGATGCGCCGGGCGGCCAAGACCATCAACTTCGGG
GTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGCTAGCCATCACTTACG
AGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTCCCCAAGGTGCGGGC
CTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTGGAGACCC
TCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTGC
GGGAGGCGGCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCG
ACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGG
CCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGAGGCCCCAAAAGAGA
GGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGGAGGGGTTATCCCC
TGGCCGTGCCCCTGGAGGTGGAGGTGGGGAACTGGCTCTCCGCCA
AGGAGGCCATTGATGGCCGCGGCGGAGGCGGGCATCATCATCATCATCATTAA

SEQ ID NO: 125 The amino acid sequence of Sso7d-Taq fusion protein.

MITNSSATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDA PKELLQMLEKQKKGGGVTSGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGE PVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQ LALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDR IHVLHPEGYLITPAWLWEKYGLR. PDQWADYRALTGDESDNLPGVKGIGEKTARKLL EEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREP DRERLRAFLERLEFGSLLHEFGLLESPKALEEAPWPPPEGAFVGFVLSRKEPMWADL LALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLA YLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREV ERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDOL ERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPL PDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQIRJRRAFIAEEGWLLVA LDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTI NFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETL FGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGA RMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKE **GIDGRGGGGHHHHHH**

SEQ ID NO: 126 The DNA sequence encoding the Pfu-Sso7d fusion protein

ATGATTTTAGATGTGGATTACATAACTGAAGAAGGAAAACCTGTTATTAGGCTAT TCAAAAAGGGGAAAATTTAAGATAGAGCATGATAGAACTTTTAGACCAT ACATTTACGCTCTTCTCAGGGATGATTCAAAGATTGAAGAAGTTAAGAAAATAAC GGGGGAAAGGCATGGAAAGATTGTGAGAATTGTTGATGTAGAAAGGTTGAGAA AAAGTTTCTCGGCAAGCCTATTACCGTGTGGAAACTTTATTTGGAACATCCCCAA GATGTTCCCACTATTAGAGAAAAGTTAGAGAACATCCAGCAGTTGTGGACATCT TCGAATACGATATTCCATTTGCAAAGAGATACCTCATCGACAAAGGCCTAATACC AATGGAGGGGAAGAAGAGCTAAAGATTCTTGCCTTCGATATAGAAACCCTCTA TCACGAAGGAGAAGAGTTTGGAAAAGGCCCAATTATAATGATTAGTTATGCAGA TGAAAATGAAGCAAAGGTGATTACTTGGAAAAACATAGATCTTCCATACGTTGA GGTTGTATCAAGCGAGAGAGAGATGATAAAGAGATTTCTCAGGATTATCAGGGA GAAGGATCCTGACATTATAGTTACTTATAATGGAGACTCATTCGACTTCCCATAT TTAGCGAAAAGGGCAGAAAAACTTGGGATTAAATTAACCATTGGAAGAGATGGA AGCGAGCCCAAGATGCAGAGAATAGGCGATATGACGGCTGTAGAAGTCAAGGG AAGAATACATTTCGACTTGTATCATGTAATAACAAGGACAATAAATCTCCCAACA TACACACTAGAGGCTGTATATGAAGCAATTTTTGGAAAGCCAAAGGAGAAGGTA TACGCCGACGAGATAGCAAAAGCCTGGGAAAGTGGAGAGAACCTTGAGAGAGTT GCCAAATACTCGATGGAAGATGCAAAGGCAACTTATGAACTCGGGAAAGAATTC CTTCCAATGGAAATTCAGCTTTCAAGATTAGTTGGACAACCTTTATGGGATGTTT AAAGAAACGAAGTAGCTCCAAACAAGCCAAGTGAAGAGGAGTATCAAAGAAGG

CTCAGGGAGAGCTACACAGGTGGATTCGTTAAAGAGCCAGAAAAGGGGTTGTGG GAAAACATAGTATACCTAGATTTTAGAGCCCTATATCCCTCGATTATAATTACCC ACAATGTTTCTCCCGATACTCTAAATCTTGAGGGATGCAAGAACTATGATATCGC TCCTCAAGTAGGCCACAAGTTCTGCAAGGACATCCCTGGTTTTATACCAAGTCTC TTGGGACATTTGTTAGAGGAAAGACAAAAGATTAAGACAAAAATGAAGGAAACT TTAGCAAATTCTTTCTACGGATATTATGGCTATGCAAAAGCAAGATGGTACTGTA AGGAGTGTGCTGAGAGCGTTACTGCCTGGGGAAGAAGTACATCGAGTTAGTAT GGAAGGAGCTCGAAGAAAAGTTTGGATTTAAAGTCCTCTACATTGACACTGATG GTCTCTATGCAACTATCCCAGGAGGAGAAAGTGAGGAAATAAAGAAAAAGGCTC TAGAATTTGTAAAATACATAAATTCAAAGCTCCCTGGACTGCTAGAGCTTGAATA TGAAGGGTTTTATAAGAGGGGATTCTTCGTTACGAAGAAGAGGTATGCAGTAAT AGATGAAGAAGGAAAAGTCATTACTCGTGGTTTAGAGATAGTTAGGAGAGATTG GAGTGAAATTGCAAAAGAAACTCAAGCTAGAGTTTTGGAGACAATACTAAAACA CGGAGATGTTGAAGAAGCTGTGAGAATAGTAAAAGAAGTAATACAAAAGCTTGC CAATTATGAAATTCCACCAGAGAAGCTCGCAATATATGAGCAGATAACAAGACC ATTACATGAGTATAAGGCGATAGGTCCTCACGTAGCTGTTGCAAAGAAACTAGCT GCTAAAGGAGTTAAAATAAAGCCAGGAATGGTAATTGGATACATAGTACTTAGA GGCGATGGTCCAATTAGCAATAGGGCAATTCTAGCTGAGGAATACGATCCCAAA AAGCACAAGTATGACGCAGAATATTACATTGAGAACCAGGTTCTTCCAGCGGTA CTTAGGATATTGGAGGGATTTGGATACAGAAAGGAAGACCTCAGATACCAAAAG ACAAGACAAGTCGGCCTAACTTCCTGGCTTAACATTAAAAAATCCGGTACCGGC GGTGGCGTGCAACCGTAAAGTTCAAGTACAAAGGCGAAGAAAAAGAGGTAGA CATCTCCAAGATCAAGAAAGTATGGCGTGTGGGCAAGATGATCTCCTTCACCTAC GACGAGGCGGTGGCAAGACCGCCGTGGTGCGGTAAGCGAAAAGGACGCGCC GAAGGAGCTGCTGCAGATGCTGGAGAAGCAGAAAAAGTGA

SEQ ID NO: 127 The amino acid sequence of the Pfu-Sso7d fusion protein

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERH GKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFA KRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNID LPYVEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS EPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEI AKAWESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGN LVEWFLLRKAYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFR ALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTK MKETQDPIEKILLDYRQKAIKLLANSFYGYYGYAKARWYCKECAESVTAWGRKYIE LVWKELEEKFGFKVLYIDTDGLYATIPGGESEEIKKKALEFVKYINSKLPGLLELEYE GFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRDWSEIAKETQARVLETILKHGDVEE AVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAKGVKIKPG MVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAEYYIENQVLPAVLRILEGFGYRKED LRYQKTRQVGLTSWLNIKKSGTGGGGATVKFKYKGEEKEVDISKIKKVWRVGKMIS FTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

SEQ ID NO: 128 The DNA sequence encoding the Sac7d-ΔTaq fusion protein

```
gagaggcccc tttccgctgt cctggcccac atggaggcca cgggggtgcg cctggacgtg
gcctatctca gggccttgtc cctggaggtg gccgaggaga tcgcccgcct cgaggccgag
gtcttccgcc tggccggcca ccccttcaac ctcaactccc gggaccagct ggaaagggtc
ctctttgacg agctagggct tcccgccatc ggcaagacgg agaagaccgg caagcgctcc
accagegeeg cegteetgga ggeeeteege gaggeeeace ceategtgga gaagateetg
cagtaccggg agctcaccaa gctgaagagc acctacattg accccttgcc ggacctcatc
caccccagga cgggccgcct ccacacccgc ttcaaccaga cggccacggc cacgggcagg
ctaagtagct ccgatcccaa cctccagaac atccccgtcc gcaccccgct tggqcaqaqq
atccgccggg ccttcatcgc cgaggagggg tggctattgg tggccctgga ctatagccag
atagagetea gggtgetgge ceacetetee ggegaegaga acetgateeg ggtetteeag
gaggggggg acatccacac ggagaccgcc agctggatgt tcggcgtccc ccgggaggcc
gtggaccccc tgatgcgccg ggcggccaag accatcaact tcggggtcct ctacggcatg
teggeceace geeteteeca ggagetagee atecettacg aggaggeeca ggeetteatt
gagcgctact ttcagagctt ccccaaggtg cgggcctgga ttgagaagac cctggaggag
ggcaggaggc gggggtacgt ggagaccctc ttcggccgcc gccgctacgt gccagaccta
gaggcccggg tgaagagcgt gcgggaggcg gccgagcgca tggccttcaa catgcccgtc
cagggcaccg ccgccgacct catgaagctg gctatggtga agctcttccc caggctggag
gaaatggggg ccaggatgct ccttcaggtc cacgacgagc tggtcctcga ggccccaaaa
gagagggcgg aggccgtggc ccggctggcc aaggaggtca tggagggggt gtatcccctg
gccgtgcccc tggaggtgga ggtggggata ggggaggact ggctctccqc caaggaggqc
attgatggcc gcggcggagg cgggcatcat catcatcatc attaa
```

SEQ ID NO: 129 The amino acid sequence of the Sac7d-\Darage Tag fusion protein

MITNSTVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDA PKELLDMLARAEREKKGGGVTSPKALEEAPWPPPEGAFVGFVLSRKEPMWADLLAL AAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLL DPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEGEERLLWLYREVERP LSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERV LFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLI HPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDY SQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFG VLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR RRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARML LQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAKEGIDG RGGGGHHHHHH

SEQ ID NO: 130 The DNA sequence encoding the PL-ΔTaq fusion protein

ATGATTACGAATTCGAAGAAAAAGAAAAAGAAAAAGCGTAAGAAACGCAAAAA GAAAAAGAAAGGCGGCGGTGTCACTAGTGGCGCAACCGTAAAGTTCAAGTACAA AGGCGAAGAAAAGGGTAGACATCTCCAAGATCAAGAAAGTATGGCGTGTGG GCAAGATGATCTCCTTCACCTACGACGAGGGCGGTGGCAAGACCGGCCGTGGTG CGGTAAGCGAAAAGGACGCCCGAAGGAGCTGCTGCAGATGCTGGAGAAGCAG AAAAAGGCCGCGTGTCACCAGTCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC CCGCCGGAAGGGCCTTCGTGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGG CCGATCTTCTGGCCCTGGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCG AGCCTTATAAAGCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAG ACCTGAGCGTTCTGGCCCTGAGGGAAGGCCTTGGCCTCCCGCCGGCGACGACCC CATGCTCCTCGCCTACCTCCTGGACCCTTCCAACACCACCCCCGAGGGGGTGGCC CGGCGCTACGGCGGGGGGTGGACGGAGGAGGCGGGGGGGCCGCCCTTTCC GAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTTGAGGGGGAGGAGGCTCCTT TGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTCCTGGCCCACATGGAGG CCACGGGGTGCCCTGGACGTGGCCTATCTCAGGGCCTTGTCCCTGGAGGTGGC AACCTCAACTCCCGGGACCAGCTGGAAAGGGTCCTCTTTGACGAGCTAGGGCTTC CCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCC TGGAGGCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATCCTGCAGTACCGGG

AGCTCACCAAGCTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCC CAGGACGGCCGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGCCAG GCTAAGTAGCTCCGATCCCAACCTCCAGAACATCCCCGTCCGCACCCCGCTTGGG CAGAGGATCCGCCGGGCCTTCATCGCCGAGGAGGGGTGGCTATTGGTGGCCCTG GACTATAGCCAGATAGAGCTCAGGGTGCTGGCCCACCTCTCCGGCGACGAGAAC CTGATCCGGGTCTTCCAGGAGGGGGGGGACATCCACACGGAGACCGCCAGCTGG ATGTTCGGCGTCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGGGCGGCCAAG ACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAGGAGC TAGCCATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTT CCCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGCAGGAGGCGGG GGTACGTGGAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCC GGGTGAAGAGCGTGCGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCC AGGGCACCGCCGACCTCATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCT GGAGGAAATGGGGCCAGGATGCTCCTTCAGGTCCACGACGAGCTGGTCCTCGA GGCCCCAAAAGAGAGGGCGGAGGCCGTGGCCCGGCTGGCCAAGGAGGTCATGG AGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAGGTGGGGATAGGGGAGG ATCATCATCATTAA

SEO ID NO: 131 The amino acid sequence of PL-ΔTag fusion protein

MITNSKKKKKKKKKKKKKKKKKGGGVTSGATVKFKYKGEEKEVDISKIKKVWRVGK
MISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKKGGGVTSPKALEEAPWPPPEG
AFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVL
ALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFAN
LWGRLEGEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLE
AEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIV
EKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTP
LGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMF
GVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVR
AWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAAD
LMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPL
AVPLEVEVGIGEDWLSAKEGIDGRGGGGHHHHHHH

SEQ ID NO: 132 PRIMER L71F 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 133 PRIMER L71R 5'-GCACAGCGGCTGGCTGAGGA-3'

SEQ ID NO: 134 PRIMER L18015F 15 5'-TGACGGAGGATAACGCCAGCAG-3'

SEQ ID NO: 135 PRIMER L23474R 5'-GAAAGACGA TGGGTCGCTAATACGC-3'

SEO ID NO: 136 PRIMER L18015F 5'-TGACGGAGGATAAC GCCAGCAG-3'

SEQ ID NO: 137 PRIMER L29930R 5'-GGGGTTGGAGGTCAATGGGTTC-3'

SEQ ID NO: 138 PRIMER L3035OF 5'-CCTGCTCTGCCGCTTCACGC-3'

SEQ ID NO: 139 PRIMER L3512IR 30 5'- CACATGGTACAGCAAGCCTGGC-3'

SEQ ID NO: 140 PRIMER L2089F 5'-CCCGTATCTGCTGGGA TACTGGC-3'

SEQ ID NO: 141 PRIMER L7112R 5'-CAGCGGTGCTGACTGAATCATGG-3'

SEQ ID NO: 142 PRIMER L3035OF 5 5'-CCTGCCTGCCGCTTCACGC-3'

SEQ ID NO: 143 PRIMER L40547R 5'-CCAATACCCGTTTCA TCGCGGC-3'

SEQ ID NO: 144 PRIMER H-Amelo-Y 5'-CCACCTCATCCTGG GCACC-3'

SEQ ID NO: 145 PRIMER H-Amelo-YR 5'-GCTTGAGGCCAACCATCAGAGC-3'

SEQ ID NO: 146 Human beta-globin primer 536F 5'-GGTTGGCCAATCTACTCCCAGG-3'

SEQ ID NO: 147 Human beta-globin primer 536R 5'-GCTCACTCAGTGTGGCAAAG-3'

SEQ ID NO: 148 Human beta-globin primer 1408R 5'-GATTAGCAAAAGGGCCTAGCTTGG- 3'

MARKED UP VERSION OF AMENDED FIGURE 20

Please replace Figure 20 with the replacement Figure below, which is marked up by way of bracketing and DOUBLE underlining to show the changes relative to the previous version of Figure 20.

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I AMINO ACID SEQUENCE (SEQ ID NO: 62) Met Ile Leu Asp Val Asp Tyr Ile Thr Glu Glu Gly Lys Pro Val Ile 1 5 15 Arg Leu Phe Lys Lys Glu Asn Gly Lys Phe Lys Ile Glu His Asp Arg Thr Phe Arg Pro Tyr Ile Tyr Ala Leu Leu Arg Asp Asp Ser Lys Ile 40 Glu Glu Val Lys Lys Ile Thr Gly Glu Arg His Gly Lys Ile Val Arg 50 55 60 Ile Val Asp Val Glu Lys Val Glu Lys Lys Phe Leu Gly Lys Pro Ile 65 70 80 Thr Val Trp Lys Leu Tyr Leu Glu His Pro Gln Asp Val Pro Thr Ile 85 90 95 Arg Glu Lys Val Arg Glu His Pro Ala Val Val Asp Ile Phe Glu Tyr 100 105 110 Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro 115 120 125 Met Glu Gly Glu Glu Leu Lys Ile Leu Ala Phe Asp Ile Glu Thr Leu Tyr His Glu Gly Glu Glu Phe Gly Lys Gly Pro Ile Ile Met Ile 150 145 155 160 Ser Tyr Ala Asp Glu Asn Glu Ala Lys Val Ile Thr Trp Lys Asn Ile 165 170 175

Asp Leu Pro Tyr Val Glu Val Val Ser Ser Glu Arg Glu Met Ile Lys
180 185 190

Arg Phe Leu Arg Ile Ile Arg Glu Lys Asp Pro Asp Ile Ile Val Thr

195 200 205

Tyr Asn Gly Asp Ser Phe Asp Phe Pro Tyr Leu Ala Lys Arg Ala Glu 210 215 220

Lys Leu Gly Ile Lys Leu Thr Ile Gly Arg Asp Gly Ser Glu Pro Lys 225 230 235 240

Met Gln Arg Ile Gly Asp Met Thr Ala Val Glu Val Lys Gly Arg Ile 245 250 255

His Phe Asp Leu Tyr His Val Ile Thr Arg Thr Ile Asn Leu Pro Thr 260 265 270

Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Lys Pro Lys Glu 275 280 285

Lys Val Tyr Ala Asp Glu Ile Ala Lys Ala Trp Glu Ser Gly Glu Asn 290 295 300

Leu Glu Arg Val Ala Lys Tyr Ser Met Glu Asp Ala Lys Ala Thr Tyr 305 310 315 320

Glu Leu Gly Lys Glu Phe Leu Pro Met Glu Ile Gln Leu Ser Arg Leu 325 330 335

Val Gly Gln Pro Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu 340 345 350

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Val Ala 355 360 365

Pro Asn Lys Pro Ser Glu Glu Glu Tyr Gln Arg Arg Leu Arg Glu Ser 370 380

Tyr 385	Thr	Gly	Gly	Phe	Val 390	Lys	Glu	Pro	Glu	Lys 395	Gly	Leu	Trp	Glu	Asn 400
Ile	Val	Tyr	Leu	Asp 405	Phe	Arg	Ala	Leu	Tyr 410	Pro	Ser	Ile	Ile	Ile 415	Thr
His	Asn	Val	Ser 420	Pro	Asp	Thr	Leu	Asn 425	Leu	Glu	Gly	Cys	Lys 430	Asn	Tyr
Asp	Ile	Ala 435	Pro	Gln	Val	Gly	His 440	Lys	Phe	Cys	Lys	Asp 445	Ile	Pro	Gly
Phe	Ile 450	Pro	Ser	Leu	Leu	Gly 455	His	Leu	Leu	Glu	Glu 460	Arg	Gln	Lys	Ile
Lys 465	Thr	Lys	Met	Lys	Glu 470	Thr	Gln	Asp	Pro	Ile 475	Glu	Lys	Ile	Leu	Leu 480
Asp	Tyr	Arg	Gln	Lys 485	Ala	Ile	Lys	Leu	Leu 490	Ala	Asn	Ser	Phe	Tyr 495	Gly
Tyr	Tyr	Gly	Tyr 500	Ala	Lys	Ala	Arg	Trp 505	Tyr	Cys	Lys	Glu	Cys 510	Ala	Glu
Ser	Val	Thr 515	Ala	Trp	Gly	Arg	Lys 520	Tyr	Ile	Glu	Leu	Val 525	Trp	Lys	Glu
Leu	Glu 530	Glu	Lys	Phe	Gly	Phe 535	Lys	Val	Leu	Tyr	Ile 540	Asp	Thr	Asp	Gly
Leu 545	Tyr	Ala	Thr	Ile	Pro 550	Gly	Gly	Glu	Ser	Glu 555	Glu	Ile	Lys	Lys	Lys 560
Ala	Leu	Glu	Phe	Val 565	Lys	Tyr	Ile	Asn	Ser 570	Lys	Leu	Pro	Gly	Leu 575	Leu
Glu	Leu	Glu	Tyr 580	Glu	Gly	Phe	Tyr	Lys 585	Arg	Gly	Phe	Phe	Val 590	Thr	Lys

Lys Arg Tyr Ala Val Ile Asp Glu Glu Gly Lys Val Ile Thr Arg Gly Leu Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala Arg Val Leu Glu Thr Ile Leu Lys His Gly Asp Val Glu Glu Ala Val Arg Ile Val Lys Glu Val Ile Gln Lys Leu Ala Asn Tyr Glu Ile Pro Pro Glu Lys Leu Ala Ile Tyr Glu Gln Ile Thr Arg Pro Leu His Glu Tyr Lys Ala Ile Gly Pro His Val Ala Val Ala Lys Lys Leu Ala Ala Lys Gly Val Lys Ile Lys Pro Gly Met Val Ile Gly Tyr Ile Val Leu Arg Gly Asp Gly Pro Ile Ser Asn Arg Ala Ile Leu Ala Glu Glu Tyr Asp Pro Lys Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln Val Leu Pro Ala Val Leu Arg Ile Leu Glu Gly Phe Gly Tyr Arg Lys Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Thr Ser

Trp Leu Asn Ile Lys Lys Ser
770 775

PURIFIED THERMOSTABLE PYROCOCCUS FURIOSUS DNA POLYMERASE I NUCLEOTIDE SEQUENCE (SEQ ID NO: 61)

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